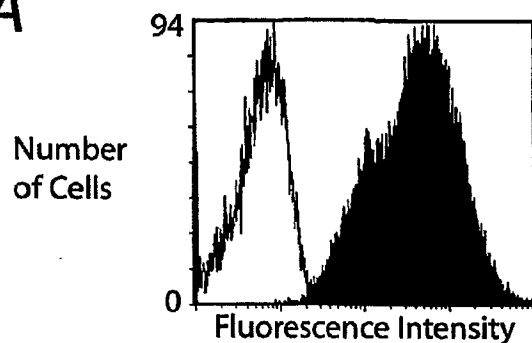


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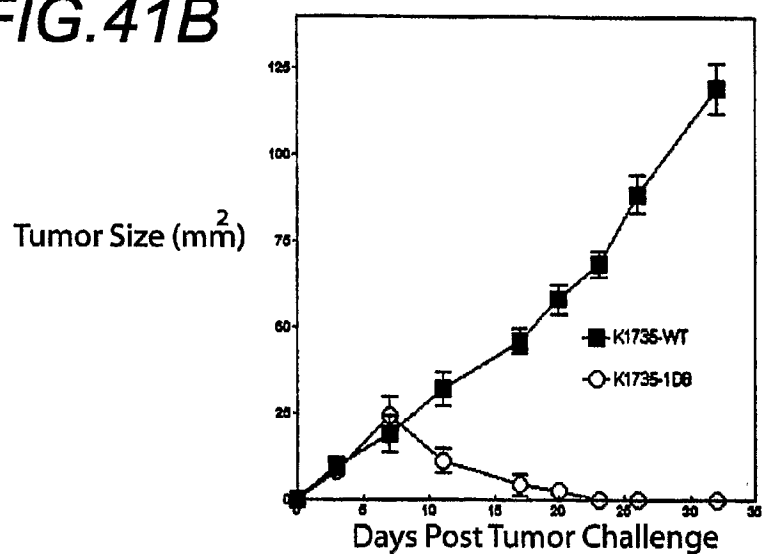
PCT/US2003/024918

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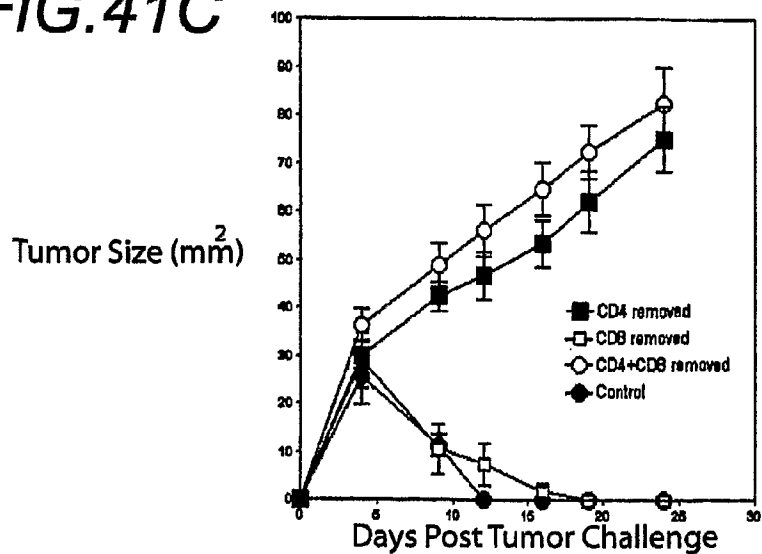
**FIG.41A**



**FIG.41B**

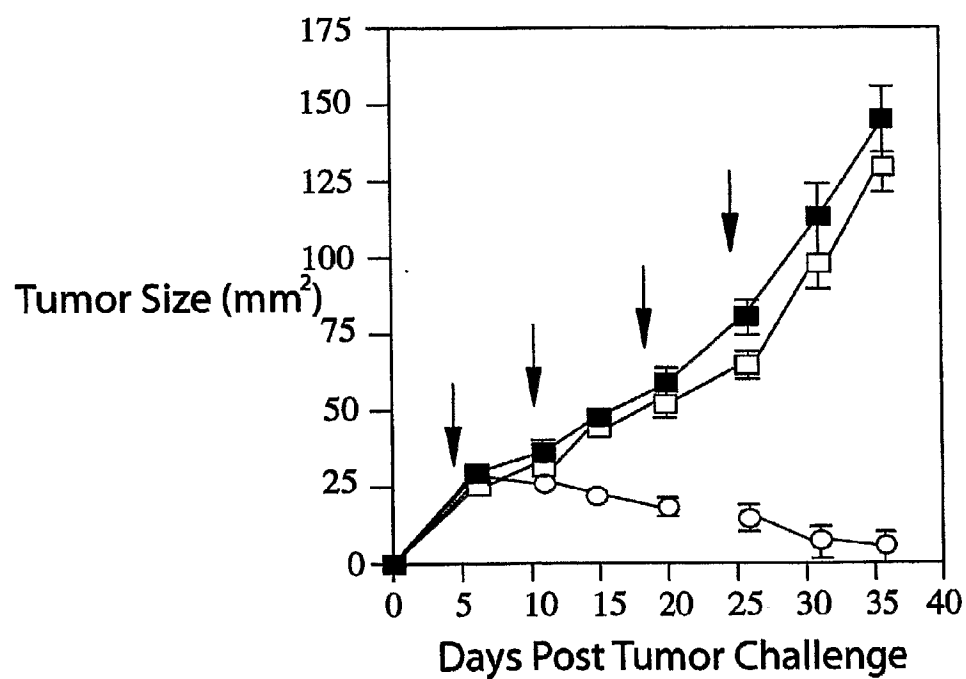


**FIG.41C**



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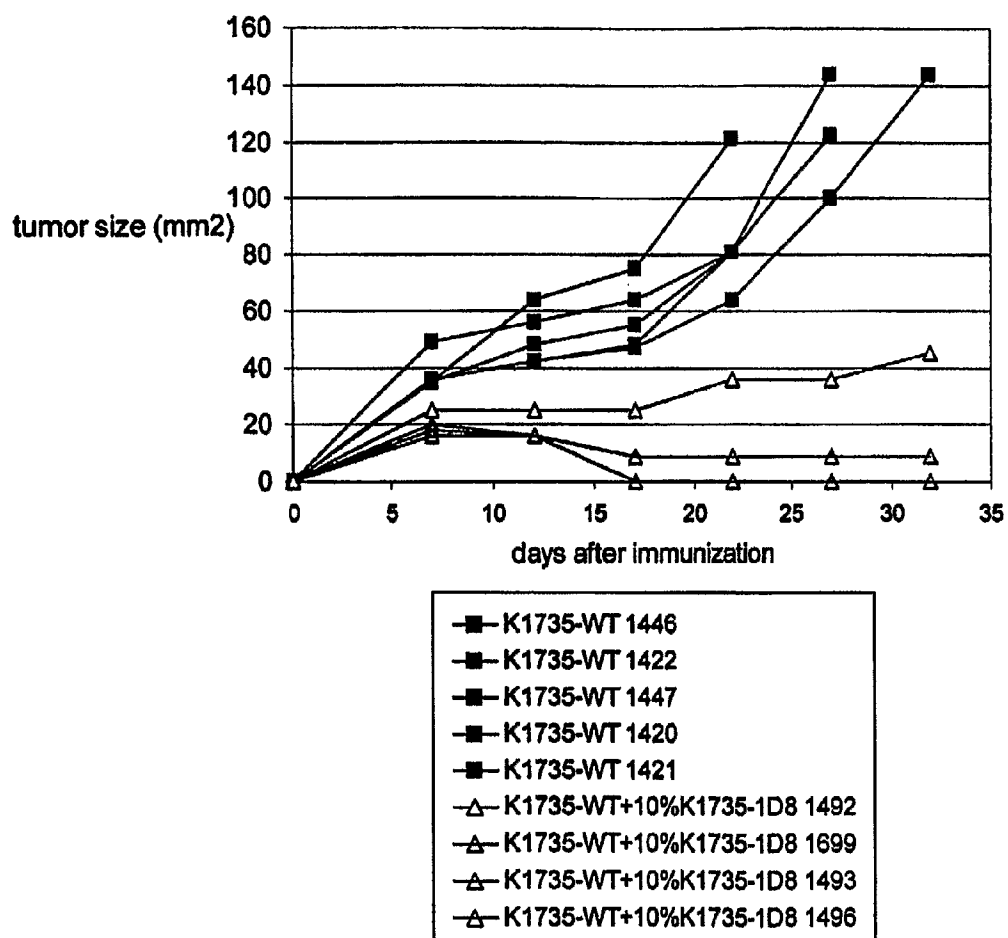
**FIG. 42**



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# FIG.43

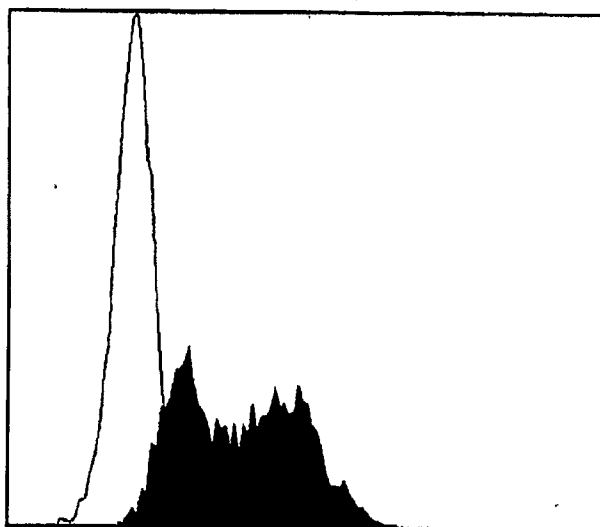
Mixtures of K1735-WT and K1735-1D8 transfected tumor lines  
inhibit tumor outgrowth in C3H mice



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## FIG. 44

Expression of Anti-CD137 scFvlg on the Surface of  
Panned Ag104 Transfected Tumor Cells

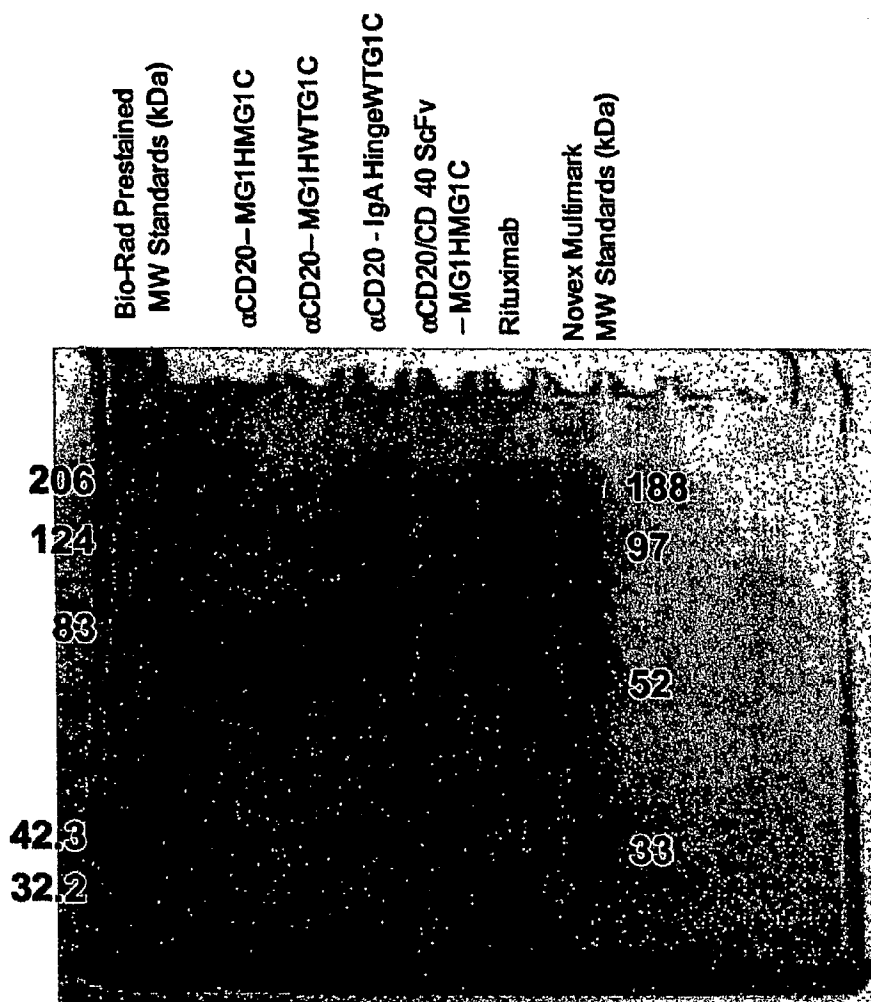


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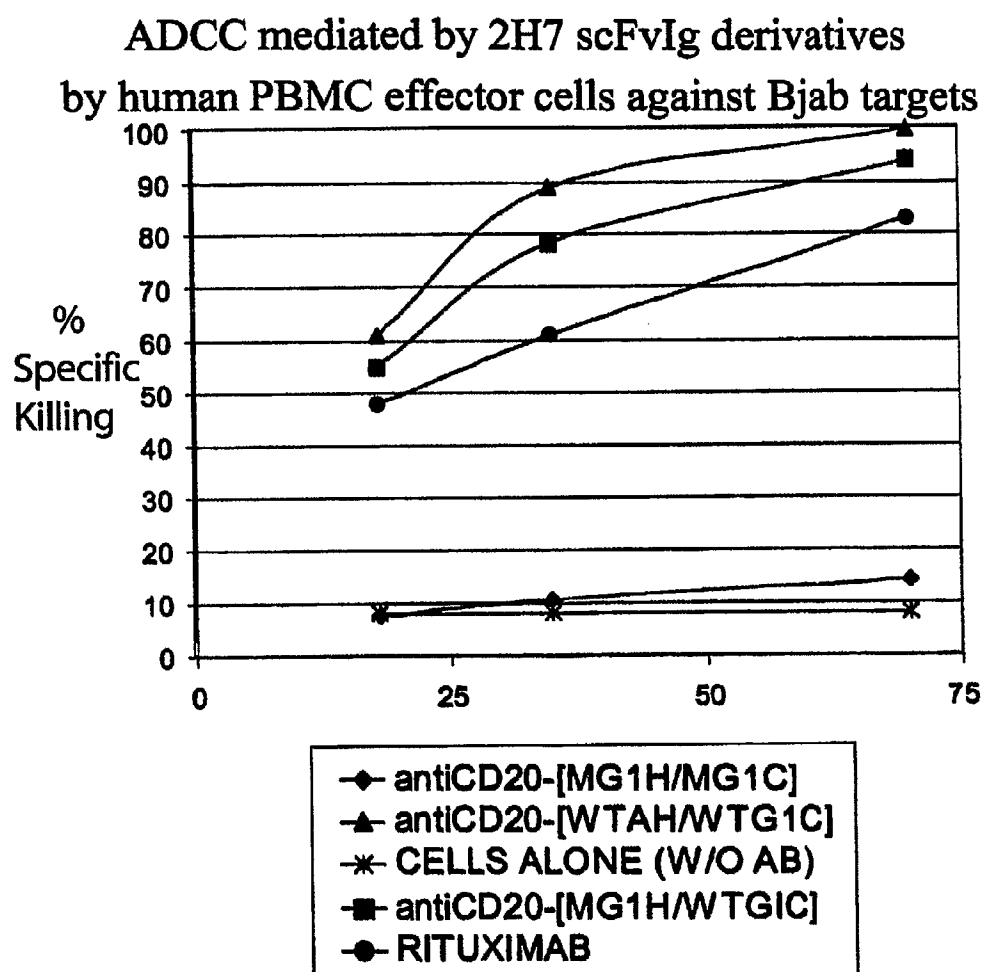
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**FIG.45**



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**FIG.46**



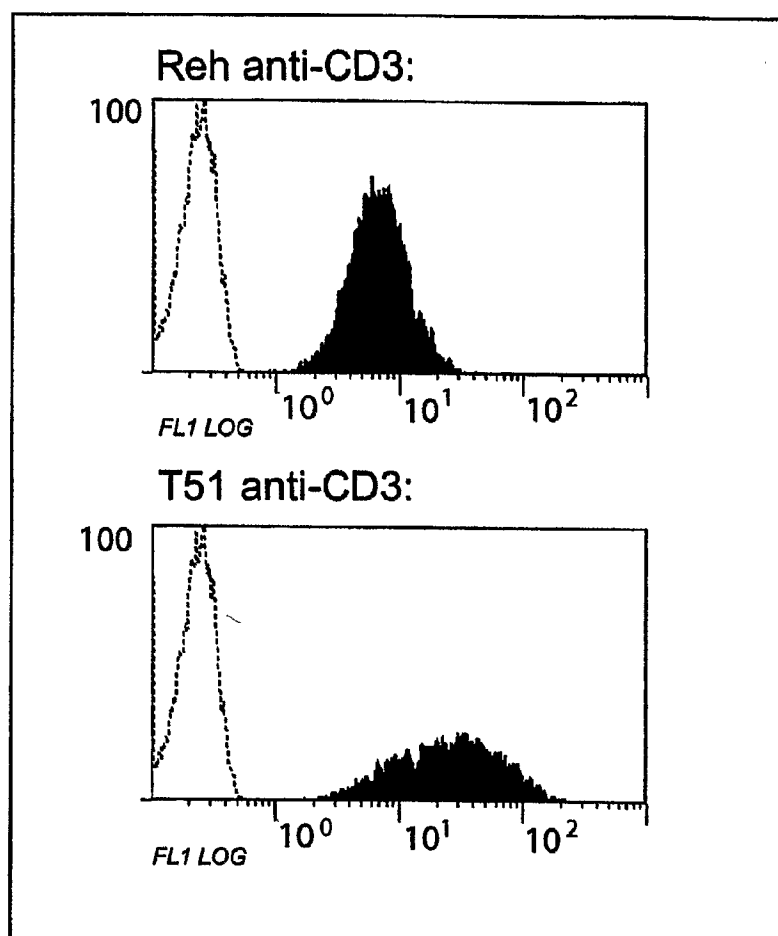
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## FIG.47

Cell surface expression of anti-human CD3 scFvIg fusion protein on Reh and T51 Cells.

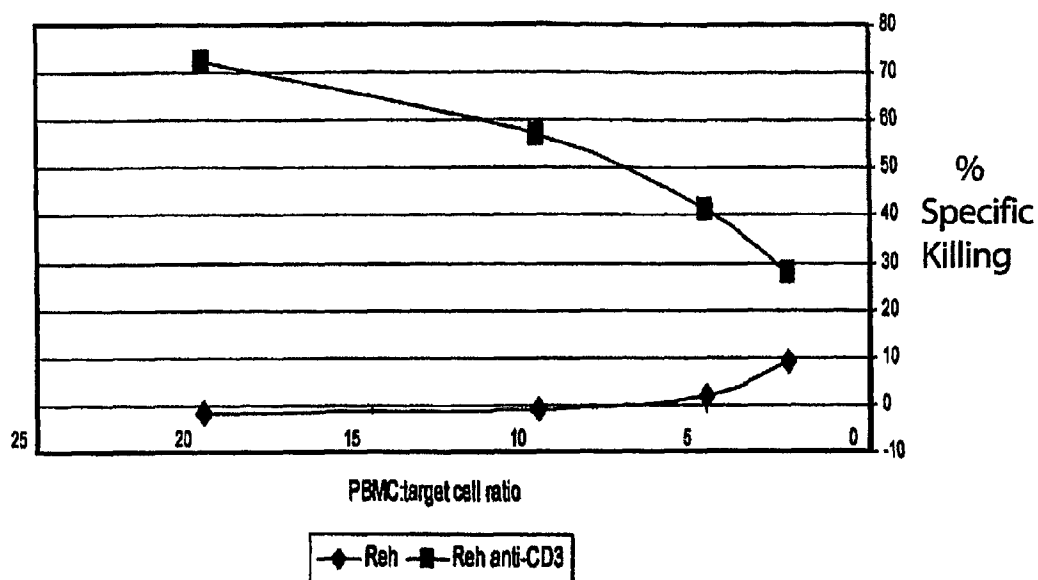


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# FIG.48A

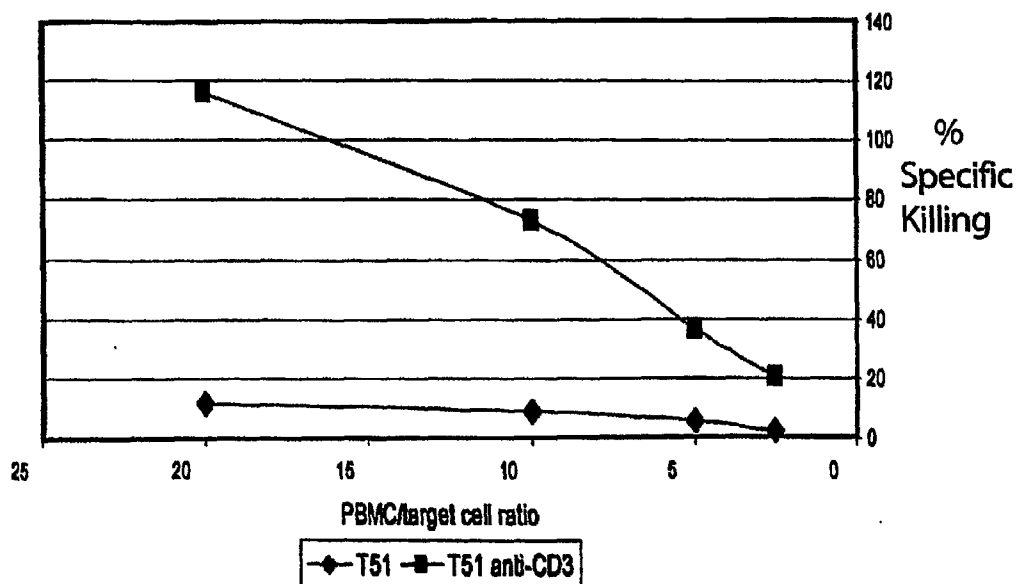
Targeting of Cytotoxicity to Transfected Cell Lines  
by Surface expression of CD3 scFvIg

Cytotoxic activity of resting PBMC towards transfected Reh cells



# FIG.48B

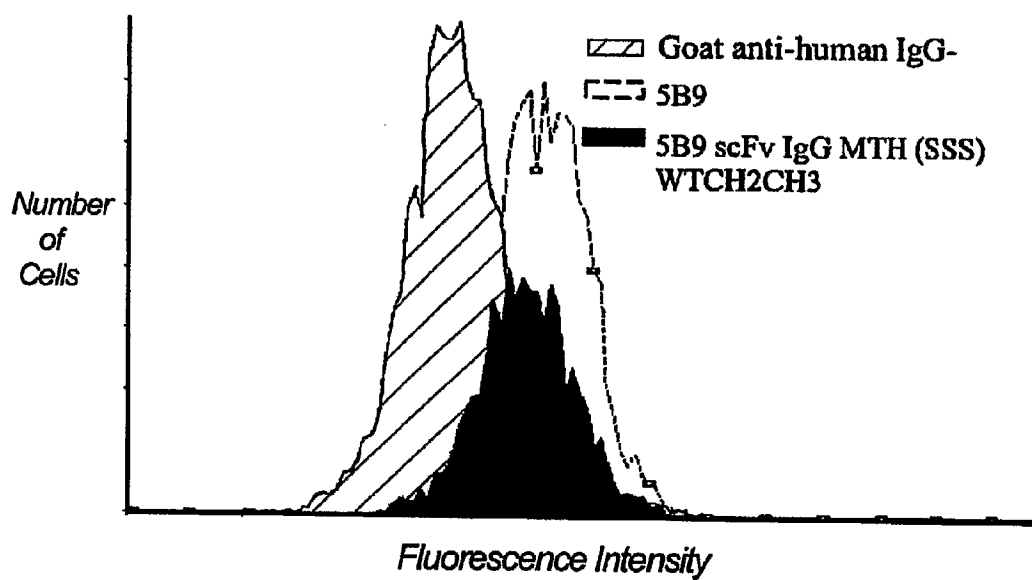
Cytotoxic activity of resting PBMC towards transfected T51 lymphoblastoid cells





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**FIG.49**



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<160> 426

<170> PatentIn version 3.0

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<222> (79)..(396)

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<220>

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120

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180

taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct  
240

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300

agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca  
360

cccacgttcg gtgctgggac caagctggag ctgaaagggt gcggtggctc gggcggtggt  
420

ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggtg

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600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta
660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg
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120
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660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg
720
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<223> HINGE CYSTEINES (826-829; 844-847; 853-856) MUTATED TO SERINES  
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FUNCTION

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60  
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120  
ccaggggaga aggtcacaaat gacttgcaagg gccagctcaa gtgtaagtta catgcactgg  
180  
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct  
240  
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300  
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca  
360  
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcgggtggctc gggcgggtgt  
420  
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<220>  
<221> C\_region  
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180  
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct  
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660  
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<220>  
<221> C\_region  
<222> (865)..(1518)  
<223> HUMAN IGG1 CH2 AND CH3 WILD TYPE FC DOMAIN

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360  
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<222> (70)..(723)  
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gtgtacaccc tgcccccac ccgggatgag ctgaccaaga accaggtcag cctgacctgc  
480  
ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg  
540  
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac  
600  
agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg  
660  
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa  
720  
tgatctaga  
729

<210> 8  
<211> 825  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> SYNTHETIC MOUSE SCFV FUSION GENE

<220>  
<221> misc\_feature  
<222> (13)..(72)  
<223> LIGHT CHAIN LEADER PEPTIDE



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<220>  
<221> V\_region  
<222> (73)..(405)  
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

<220>  
<221> misc\_feature  
<222> (406)..(450)  
<223> SYNTHETIC (GLY4SER)3 LINKER PEPTIDE

<220>  
<221> V\_region  
<222> (454)..(825)  
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

<400> 8  
aagcttgccg ccatggagac agacacactc ctgctatggg tgctgctgct ctgggttcca  
60  
ggctccactg gtgacattgt gctgaccaa tctccagctt ctttggtgt gtctctaggg  
120  
cagagggcca ccatctctg caaggccagc caaagtgttg attatgatgg tgatagttat  
180  
ttgaactggt accaacagat tccaggacag ccacccaaac tcctcatcta tgatgcatcc  
240  
aatctagttt ctgggatccc acccaggttt agtggcagtg ggtctgggac agacttcacc  
300  
ctcaacatcc atcctgtgga gaagggtgat gctgcaacct atcactgtca gcaaagtact  
360  
gaggatccgt ggacgttcgg tggaggcacc aagctggaaa tcaaagggtg cggtggctcg  
420  
ggcgggtgtg ggtcgggtgg cggcggatcg tcacaggttc agctgcagca gtctggggct  
480  
gagctgtga ggcctgggtc ctgagtgaa atttctgca aggccttctg ctatgcattc  
540  
agtagctact ggatgaactg ggtgaagcag aggcctggac agggcttga gtggattgga  
600  
cagatttggc ctggagatgg tgatactaac tacaatggaa agttcaaggg taaagccact  
660  
ctgactgcag acgaatcctc cagcacagcc tacatgcaac tcagcagcct agcatctgag  
720  
gactctgcgg tctatttctg tgcaagacgg gagactacga cggtaggccg ttattactat  
780  
gctatggact actgggtgca aggaacctca gtcaccgtct cctca  
825

<210> 9  
<211> 795  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> SYNTHETIC MOUSE SCFV FUSION GENE

<220>  
<221> misc\_feature  
<222> (13)..(72)  
<223> LIGHT CHAIN LEADER PEPTIDE SEQUENCE

<220>  
<221> V\_region  
<222> (73)..(393)  
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

<220>  
<221> misc\_feature  
<222> (394)..(441)  
<223> SYNTHETIC LINKER PEPTIDE ENCODED (GLY4SER)3

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<220>
<221> V_region
<222> (442)..(795)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

<400> 9
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ggtggcagat gtgacatcca gatgactcag tctccagcct ccctatctgc atctgtggga
120
gagactgtca ccatcacatg tcgaacaagt gaaaatgttt acagttatatt ggcttgggtat
180
cagcagaaac agggaaaatc tcctcagctc ctgggtctctt ttgcaaaaac cttagcagaa
240
ggtgtgcat caagggtcag tggcagtga tcaggcacac agttttctct gaagatcagc
300
agcctgcagc ctgaagattc tggaagttat ttctgtcaac atcattccga taatccgtgg
360
acgttcggtg gaggcaccga actggagatc aaagggtggcg gtggctcggg cgggtgggtggg
420
tcgggtggcg gcggatcgtc agcgggtccag ctgcagcagt ctggacctga gctggaaaag
480
cctggcgctt cagtgaagat ttcctgcaag gcttctgggt actcattcac tggctacaat
540
atgaactggg tgaagcagaa taatggaaa agccttgagt ggattggaaa tattgatcct
600
tattatggtg gtactaccta caaccggaag ttcaaggga aggccacatt gactgtagac
660
aaatcctcca gcacagccta catgcagctc aagagtctga catctgagga ctctgcagtc
720
tattactgtg caagatcggg cggccctatg gactactggg gtcaaggaac ctgagtcacc
780
gtctcttctg atcag
795

<210> 10
<211> 824
<212> DNA
<213> Artificial Sequence

<220>
<223> SYNTHETIC MOUSE FUSION GENE

<220>
<221> sig_peptide
<222> (1)..(61)
<223> native light chain leader peptide

<220>
<221> V_region
<222> (62)..(397)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>
<221> misc_feature
<222> (398)..(445)
<223> (gly4ser)3 linker peptide

<220>
<221> V_region
<222> (445)..(818)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>
<221> misc_feature
<222> (819)..(824)
<223> BclI restriction site

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<400> 10
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60
aacattatga tgacacagtc gccatcatct ctggctgtgt cagcaggaga aaaggtcact
120
atgaactgta agtccagtc aagtgttttc tacagttcaa atcagaggaa ttatttggcc
180
tggtatcagc agaaaccagg gcagtctccc aaattgctga tctactgggc atctactagg
240
gaatctggtg tccctgatcg cttcacaggc agtggatccg ggacagactt tactcttacc
300
atcagcagtg tacatactga agacctggca gtttattact gtcataaatt cctctcttcg
360
tggaagtctg gtggaggcac caagctggaa atcaaaggcg gtggtggttc ggggtgggtg
420
ggttcgggtg gcggcggatc ttctcaggtc caactgcagc agcctggggc tgaactgggtg
480
aagcctggga cttcagtga gctgtcctgc aaggcctctg gctacacctt caccaactac
540
tggaagtctt ggggtgaagca gacgcctgga gaaggccttg agtggattgg agaaattatt
600
cctagcaacg gtcgtactaa atacaatgag aagttcaaga gcaaggccac actgactgca
660
gacaaatcct cccgcacagc ctacatgcaa ctacagagcc tggcatctga ggactctgcg
720
gtctattatt gtgcaagaga gatgtccatt attactacgg tactgactcc cggtttgctt
780
actggggcca agggactctg gtcactgtct ctgcagcctg atca
824
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<210> 11
<211> 266
<212> PRT
<213> Mus musculus
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<220>
<221> INIT_MET
<222> (1)..(1)
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<220>
<221> SIGNAL
<222> (1)..(22)
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<220>
<221> DOMAIN
<222> (23)..(128)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20
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<220>
<221> SITE
<222> (129)..(144)
<223> ASP-(GLY3SER)-(GLY4SER)2-SER LINKER PEPTIDE
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<220>
<221> DOMAIN
<222> (145)..(266)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20
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<400> 11
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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1           5           10           15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20           25           30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35           40           45
ser ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
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50	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
	Ser	Phe	Asn	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	
	115	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	
	130	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
				165	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
	Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
	195	Lys	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
	210	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe
225	Ala	Arg	Val	Val	Tyr	Tyr	Ser	Asn	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp
				245	Thr	Thr	Val	Thr	Val	Ser	Asp					
	Gly	Thr	Gly	Thr	Thr	Val	Thr	Val	Ser	Asp						
				260												

<210> 12  
 <211> 271  
 <212> PRT  
 <213> Mus musculus  
 <220>  
 <221> SITE  
 <222> (1)..(271)  
 <223> MOUSE ANTI-HUMAN CD19 SCFV

<400> 12

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1				5					10					15	
Gly	Ser	Thr	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala
			20					25					30		
Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	Gln	Ser
		35					40					45			
Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Ile	Pro
	50					55					60				
Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	Val	Ser
65				70					75					80	
Gly	Ile	Pro	Pro	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
				85				90						95	
Leu	Asn	Ile	His	Pro	Val	Glu	Lys	Val	Asp	Ala	Ala	Thr	Tyr	His	Cys
			100					105					110		
Gln	Gln	Ser	Thr	Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu
		115					120					125			
Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	130					135					140				
Gly	Ser	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg
145				150					155					160	
Pro	Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe
				165				170						175	
Ser	Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu
			180					185					190		
Glu	Trp	Ile	Gly	Gln	Ile	Trp	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn
		195					200					205			
Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Glu	Ser	Ser	Ser
	210					215					220				
Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	Ser	Ala	Val

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225 230 235 240  
Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr  
245 250 255  
Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
260 265 270

<210> 13  
<211> 259  
<212> PRT  
<213> Mus musculus

<220>  
<221> SITE  
<222> (1)..(259)  
<223> MOUSE ANTI-HUMAN CD37 SCFV

<400> 13

Met Val Ser Thr Ala Gln Phe Leu Gly Leu Leu Leu Leu Trp Leu Thr  
1 5 10 15  
Gly Gly Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser  
20 25 30  
Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Thr Ser Glu Asn  
35 40 45  
Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro  
50 55 60  
Gln Leu Leu Val Ser Phe Ala Lys Thr Leu Ala Glu Gly Val Pro Ser  
65 70 75 80  
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Ser  
85 90 95  
Ser Leu Gln Pro Glu Asp Ser Gly Ser Tyr Phe Cys Gln His His Ser  
100 105 110  
Asp Asn Pro Trp Thr Phe Gly Gly Gly Thr Glu Leu Glu Ile Lys Gly  
115 120 125  
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ala  
130 135 140  
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala Ser  
145 150 155 160  
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn  
165 170 175  
Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly  
180 185 190  
Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys  
195 200 205  
Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr Met  
210 215 220  
Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala  
225 230 235 240  
Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr  
245 250 255  
Val Ser Ser

<210> 14  
<211> 272  
<212> PRT  
<213> Mus musculus

<220>  
<221> SITE  
<222> (1)..(272)  
<223> MOUSE ANTI-HUMAN CD22 SCFV

<400> 14

Met Glu Ser His Ser Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser  
1 5 10 15  
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala

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Val	Ser	Ala	Gly	Glu	Lys	Val	Thr	Met	Asn	Cys	Lys	Ser	Ser	Gln	Ser
		20					25					30			
Val	Phe	35	Ser	Ser	Asn	Gln	40	Asn	Tyr	Leu	Ala	45	Tyr	Gln	Gln
	50				55						60				
Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg
65					70					75				80	
Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp
			85						90					95	
Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	His	Thr	Glu	Asp	Leu	Ala	Val	Tyr
			100					105					110		
Tyr	Cys	His	Gln	Phe	Leu	Ser	Ser	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		115					120					125			
Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
	130						135					140			
Gly	Gly	Ser	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val
145					150					155				160	
Lys	Pro	Gly	Thr	Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr
				165					170					175	
Phe	Thr	Asn	Tyr	Trp	Met	Val	Trp	Val	Lys	Gln	Thr	Pro	Gly	Glu	Gly
			180					185					190		
Leu	Glu	Trp	Ile	Gly	Glu	Ile	Ile	Pro	Ser	Asn	Gly	Arg	Thr	Lys	Tyr
		195					200					205			
Asn	Glu	Lys	Phe	Lys	Ser	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser
	210					215					220				
Arg	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	Ser	Ala
225					230					235				240	
Val	Tyr	Tyr	Cys	Ala	Arg	Glu	Met	Ser	Ile	Ile	Thr	Thr	Val	Leu	Thr
			245						250					255	
Pro	Gly	Leu	Leu	Thr	Gly	Ala	Lys	Gly	Leu	Trp	Ser	Leu	Ser	Leu	Gln
			260					265					270		

<210> 15

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)

<223> HUMAN IGG1 WILD TYPE HINGE, CH2, CH3 FC

<400> 15

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20					25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
		50				55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65					70					75				80	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
			85						90					95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100					105					110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
		115					120					125			

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 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys  
 260 265 270  
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 275 280 285  
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 290 295 300  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His  
 305 310 315 320  
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 325 330 335  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 340 345 350  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 355 360 365  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 370 375 380  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 385 390 395 400  
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 405 410 415  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 420 425 430  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 435 440 445  
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 450 455 460  
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 465 470 475 480  
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 485 490 495  
 Pro Gly Lys

<210> 16  
 <211> 499  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>  
 <221> SITE  
 <222> (1)..(265)  
 <223> 2H7 SCFV TARGETED TO HUMAN CD20

<220>  
 <221> DOMAIN  
 <222> (265)..(499)  
 <223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)  
 PROLINE IN CH2 MUTATED TO SERINE (AMINO ACID 290)

<400> 16

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
260 265 270
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
275 280 285
Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290 295 300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
305 310 315 320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325 330 335
His Asn Ala Lys Thr Lys Pro Arg Glu Gln Tyr Asn Ser Thr Tyr
340 345 350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355 360 365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370 375 380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385 390 395 400
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405 410 415
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420 425 430
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
435 440 445
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
450 455 460
Asp Lys Ser Arg Trp Gln Gly Asn Val Phe Ser Cys Ser Val Met
465 470 475 480
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
485 490 495
Pro Gly Lys

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<210> 17  
<211> 499  
<212> PRT



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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)  
CH2 AND CH3 DOMAINS ARE WILD TYPE IN SEQUENCE

<400> 17

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1      5      10      15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100     105     110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115     120     125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130     135     140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145     150     155     160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165     170     175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180     185     190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195     200     205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210     215     220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225     230     235     240
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245     250     255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
260     265     270
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
275     280     285
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290     295     300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
305     310     315     320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325     330     335
His Asn Ala Lys Thr Lys Pro Arg Glu Gln Tyr Asn Ser Thr Tyr
340     345     350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355     360     365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370     375     380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385     390     395     400

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
405 410 415  
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
420 425 430  
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
435 440 445  
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
450 455 460  
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
465 470 475 480  
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
485 490 495  
Pro Gly Lys

<210> 18  
<211> 505  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> MOUSE-HUMAN FUSION PROTEIN

<220>  
<221> SITE  
<222> (1)..(265)  
<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>  
<221> DOMAIN  
<222> (266)..(288)  
<223> WILD TYPE IGA HINGE

<220>  
<221> DOMAIN  
<222> (289)..(505)  
<223> HUMAN IGG1 CH2 AND CH3 DOMAINS, WILD TYPE SEQUENCE

<400> 18

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
20 25 30  
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
35 40 45  
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60  
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80  
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125  
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
130 135 140  
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175  
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
180 185 190  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
210 215 220  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr  
 Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys  
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
 Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 500 505

<210> 19  
 <211> 234  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> DOMAIN  
 <222> (1)..(234)  
 <223> MUTANT IGG1 HINGE (AMINO ACIDS 7, 13, 16)  
 WILD TYPE CH2 AND CH3 DOMAINS  
 ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<400> 19

Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser  
 1 5 10 15  
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
 20 25 30  
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
 35 40 45  
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
 50 55 60  
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
 65 70 75 80  
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
 85 90 95  
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
 100 105 110  
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
 115 120 125  
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu  
 130 135 140  
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
145 150 155 160  
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
165 170 175  
Asn Tyr Lys Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
180 185 190  
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
195 200 205  
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
210 215 220  
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
225 230

<210> 20  
<211> 240  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> (1)..(23)  
<223> ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<220>  
<221> DOMAIN  
<222> (24)..(240)  
<223> HUMAN IGG1 WILD TYPE CH2 AND CH3 FC

<400> 20

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro  
1 5 10 15  
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20 25 30  
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg  
35 40 45  
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro  
50 55 60  
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
65 70 75 80  
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val  
85 90 95  
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
100 105 110  
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
115 120 125  
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
130 135 140  
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
145 150 155 160  
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
165 170 175  
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
180 185 190  
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
195 200 205  
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
210 215 220  
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
225 230 235 240

<210> 21  
<211> 1470  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> MOUSE-HUMAN HYBRID

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<220>
<221> misc_feature
<222> (1)..(808)
<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>
<221> misc_feature
<222> (814)..(1455)
<223> HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154

<400> 21
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgtctca
60
gtcataattg ccagaggaca aattgttctc tcccagctctc cagcaatcct gtctgcatct
120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg
180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct
240
tctggagtcg ctgctcgctt cagtggcagt ggggtctggga cctcttactc tctcacaatc
300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca
360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcgggtggctc gggcggtggt
420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggtg
480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac
540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat
600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta
660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg
720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg
780
ggcacaggga ccacggtcac cgtctctgat ccaagaagg tggacaagat agaagatgaa
840
aggaatcttc atgaagattt tgtattcatg aaaacgatac agagatgcaa cacaggagaa
900
agatccttat ccttactgaa ctgtgaggag attaaaagcc agtttgaaagg ctttgtgaag
960
gatataatgt taaacaaaga ggagacgaag aaagaaaaca gctttgaaat gcaaaaagg
1020
gatcagaatc ctcaaattgc ggcacatgtc ataagtgagg ccagcagtaa aacaacatct
1080
gtgttacagt gggctgaaaa aggatactac accatgagca acaacttggg aaccttgga
1140
aatgggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtcacc
1200
ttctgttcca atcggaagc ttcgagtcaa gctccattta tagccagcct ctgcctaaag
1260
tccccgggta gattcgagag aatcttactc agagctgcaa ataccacag ttccgcaaaa
1320
ccttgcgggc aacaatccat tcaactggga ggagtatttg aattgcaacc aggtgcttcg
1380
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cacgtccttt
1440
ggcttactca aactcgagtg ataacttaga
1470

<210> 22
<211> 1290
<212> DNA
<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> MOUSE-HUMAN HYBRID

<220>

<221> misc\_feature

<222> (13)..(808)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> misc\_feature

<222> (814)..(1275)

<223> HUMAN EXTRACELLULAR DOMAIN, SHORT FORM, CD154

<400> 22

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gtcataattg ccagaggaca aattgttctc tcccagcttc cagcaatcct gtctgcatct
120
ccaggggaga aggtcacaat gacttgacag gccagctcaa gtgtaagtta catgactagg
180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct
240
tctggagtcg ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc
300
agcagagtgg aggtctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca
360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg
420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt
480
aggcctgggg cctcagtga aatgtcctgc aaggcttctg gctacacatt taccagttac
540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat
600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta
660
gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgag
720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg
780
ggcacaggga ccacgggtac cgtctctgat ccagaaaaca gctttgaaat gcaaaaagg
840
gatcagaatc ctcaaattgc ggcacatgac ataagtggag ccagcagtaa aacaacatct
900
gtgtttacag gggctgaaaa aggatactac accatgagca acaacttggg aacctggaa
960
aatgggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtcacc
1020
ttctgttcca atcgggaagc ttcgagtcga gctccattta tagccagcct ctgcctaaag
1080
tcccccggtg gattcgagag aatcttactc agagctgcaa ataccacag ttccgccaaa
1140
ccttgcgggc aacaatccat tcaactggga ggagtatttg aattgcaacc aggtgcttcg
1200
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cacgtccttt
1260
ggcttactca aactcgagtg ataacttaga
1290
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<210> 23

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 23

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
gtcaagcttg ccgcatgga tttcaagtg cagatttttc agc  
43

<210> 24  
<211> 74  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 24  
gtcgtcgagc tcccacctcc tccagatcca ccaccgccc agccaccgcc acctttcagc  
60  
tccagcttgg tccc  
74

<210> 25  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 25  
gctgctgagc tctcaggctt atctacagca agtctgg  
37

<210> 26  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 26  
gttgctgat cagagacggt gaccgtgggc cc  
32

<210> 27  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 27  
gttgctggat ccagaaaaca gctttgaaat gcaa  
34

<210> 28  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<223> OLIGONUCLEOTIDE

<400> 28  
gttgtttcta gattatcact cgagtttgag taagccaaag gacg  
44

<210> 29  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 29  
gttggtcggat ccaagaaggt tggacaagat agaag  
35

<210> 30  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 30  
gtctatataa gcagagctct ggc  
23

<210> 31  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 31  
cgaggctgat cagcgagctc tagca  
25

<210> 32  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 32  
ccgcaatttg aggattctga tcacc  
25

<210> 33  
<211> 482  
<212> PRT  
<213> Artificial Sequence



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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(266)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> DOMAIN

<222> (268)..(481)

<223> EXTRACELLULAR DOMAIN, LONG FORM, HUMAN CD154

<400> 33

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1      5      10      15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100     105     110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115     120     125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130     135     140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145     150     155     160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165     170     175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180     185     190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195     200     205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210     215     220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225     230     235     240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245     250     255
Gly Thr Gly Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys
260     265     270
Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr
275     280     285
Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys
290     295     300
Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu
305     310     315     320
Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly
325     330     335
Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
340     345     350
Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Thr Met
355     360     365
Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
370     375     380
Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
385     390     395     400
Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys
405     410     415
Ser Pro Gly Arg Phe Glu Arg Ile Leu Arg Ala Ala Asn Thr His
420     425     430

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val  
 435 440 445  
 Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro  
 450 455 460  
 ser Gln val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys  
 465 470 475 480  
 Leu Glu

<210> 34  
 <211> 422  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>  
 <221> SITE  
 <222> (1)..(266)  
 <223> MOUSE ANTI-HUMAN SCFV

<220>  
 <221> DOMAIN  
 <222> (268)..(421)  
 <223> EXTRACELLULAR DOMAIN, SHORT FORM, HUMAN CD154

<400> 34

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Pro Glu Asn Ser Phe Glu  
 260 265 270  
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser  
 275 280 285  
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly  
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325 330 335  
Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser  
340 345 350  
Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala  
355 360 365  
Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His  
370 375 380  
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn  
385 390 395 400  
Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe  
405 410 415  
Gly Leu Leu Lys Leu Glu  
420

<210> 35  
<211> 63  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> N\_region  
<222> (1)..(63)  
<223> PORTION OF HUMAN IGA HINGE DOMAIN CONTAINING ONLY 1 CYSTEINE

<400> 35  
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60  
tgc  
63

<210> 36  
<211> 21  
<212> PRT  
<213> Homo sapiens

<400> 36  
Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr  
1 5 10 15  
Pro Ser Pro Ser Cys  
20

<210> 37  
<211> 763  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(6)  
<223> BCLI SITE FOR FUSION TO AMIN TERMINAL SCFVS

<220>  
<221> N\_region  
<222> (8)..(752)  
<223> WILD TYPE IGA HINGE, CH2, CH3 DOMAINS  
TRUNCATED TO REMOVE SECRETORY COMPONENT ATTACHMENT

<400> 37  
tgatcagcca gttccctcaa ctccacctac cccatctccc tcaactccac ctaccccatc  
60  
tccctcatgc tgccaccccc gactgtcact gcaccgaccg gccctcgagg acctgctctt  
120

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 ctgtggctgc tacagcgtgt ccagtgtcct gccgggctgt gccgagccat ggaaccatgg  
 300  
 gaagaccttc acttgactg ctgcctaccc cgagtccaag accccgctaa ccgccacct  
 360  
 ctcaaaatcc ggaacacat tccggcccga ggtccacctg ctgccgccgc cgtcggagga  
 420  
 gctggccctg aacgagctgg tgacgctgac gtgcctggca cgtggcttca gcccgaagga  
 480  
 tgtgtgtgtt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg  
 540  
 ggcattcccg caggagccca gccagggcac caccaccttc gctgtgacca gcatactgcg  
 600  
 cgtggcagcc gaggactgga agaaggggga caccttctcc tgcattgtgg gccacgaggg  
 660  
 cctgccgctg gccttcacac agaagaccat cgaccgcttg gcgggtaaac ccacccatgt  
 720  
 caatgtgtct gttgtcatgg cggaggtgga ctgataatct aga  
 763

<210> 38  
 <211> 250  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> DOMAIN  
 <222> (3)..(250)  
 <223> TRUNCATED FORM, REMOVAL OF LAST THREE AMINO ACIDS THAT MEDIATE  
 ATTACHMENT TO SECRETORY COMPONENT

<400> 38

Asp	Gln	Pro	Val	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro
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Pro	Thr	Pro	Ser	Pro	Ser	Cys	Cys	His	Pro	Arg	Leu	Ser	Leu	His	Arg
			20					25					30		
Pro	Ala	Leu	Glu	Asp	Leu	Leu	Leu	Gly	Ser	Glu	Ala	Ile	Leu	Thr	Cys
		35					40					45			
Thr	Leu	Thr	Gly	Leu	Arg	Asp	Ala	Ser	Gly	Val	Thr	Phe	Thr	Trp	Thr
	50				55					60					
Pro	Ser	Ser	Gly	Lys	Ser	Ala	Val	Gln	Gly	Pro	Asp	Arg	Asp	Leu	
65					70				75					80	
Cys	Gly	Cys	Tyr	Ser	Val	Ser	Ser	Val	Leu	Pro	Gly	Cys	Ala	Glu	Pro
			85					90					95		
Trp	Asn	His	Gly	Lys	Thr	Phe	Thr	Cys	Thr	Ala	Ala	Tyr	Pro	Glu	Ser
			100					105					110		
Lys	Thr	Pro	Leu	Thr	Ala	Thr	Leu	Ser	Lys	Ser	Gly	Asn	Thr	Phe	Arg
		115					120					125			
Pro	Glu	Val	His	Leu	Leu	Pro	Pro	Ser	Glu	Glu	Leu	Ala	Leu	Asn	
		130				135				140					
Glu	Leu	Val	Thr	Leu	Thr	Cys	Leu	Ala	Arg	Gly	Phe	Ser	Pro	Lys	Asp
145					150				155					160	
Val	Leu	Val	Arg	Trp	Leu	Gln	Gly	Ser	Gln	Glu	Leu	Pro	Arg	Glu	Lys
			165					170						175	
Tyr	Leu	Thr	Trp	Ala	Ser	Arg	Gln	Glu	Pro	Ser	Gln	Gly	Thr	Thr	Thr
			180				185						190		
Phe	Ala	Val	Thr	Ser	Ile	Leu	Arg	Val	Ala	Ala	Glu	Asp	Trp	Lys	Lys
		195				200						205			
Gly	Asp	Thr	Phe	Ser	Cys	Met	Val	Gly	His	Glu	Ala	Leu	Pro	Leu	Ala
		210				215				220					
Phe	Thr	Gln	Lys	Thr	Ile	Asp	Arg	Leu	Ala	Gly	Lys	Pro	Thr	His	Val
225					230					235					240
Asn	Val	Ser	Val	Val	Met	Ala	Glu	Val	Asp						

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245 250

<210> 39  
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<213> Artificial Sequence

<220>  
<223> Linker polypeptide

<400> 39  
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1 5

<210> 40  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Sequence contained in the core hinge region of  
human IgG1.

<400> 40  
Cys Pro Pro Cys  
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<210> 41  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human IgA-derived hinge.

<400> 41  
Pro Ala Ser Pro Ser Pro Thr Pro Pro Thr Ser Pro Ser Pro Thr Pro  
1 5 10 15  
Pro Thr Ser Pro Val Pro Gln Asp  
20

<210> 42  
<211> 1593  
<212> DNA  
<213> Homo sapiens

<400> 42  
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cgaggcggcc ggagtcgccg gctagccccg gcggccgccc ccgcccagac cggacgacag 120  
gccacctcgt cggcgccgcg ccgagtcgcc gcctcgccgc caacgccaca accaccgagc 180  
acggccccct gactccgtcc agtattgatc gggagagccg gagcagctc ttccggggagc 240  
agcagtcgca cctccgggga cggccggggc agcgctcctg gcgctgctgg ctgcgctctg 300  
ccggcgaggt cgggctcttg aggaaaagaa agtttgccaa ggcacgagta acaagctcac 360  
gcagttgggc acttttgaag atcattttct cagcctccag aggatgttca ataactgtga 420  
ggtggtcctt gggaatttgg aaattaccta tgtgcagagg aattatgatc tttccttctt 480  
aaagaccatc caggaggtgg ctggttatgt cctcattgcc ctcaacacag tggagcgaat 540  
tcctttggaa aacctgcaga tcatcagagg aaatatgtac tacgaaaatt cctatgcctt 600  
agcagtccta tctaactatg atgcaataaa aaccggactg aaggagctgc ccatgagaaa 660  
tttacaggaa atcctgcagt gcgccgtgcg gttcagcaac aacctgccc tgtgcaatgt 720  
ggagagcatc cagtggcggg acatagtcag cagtgcattt ctacagcaaca tgtcgatgga 780  
cttcagaaac cacctgggca gctgcaaaaa gtgtgatcca agctgtccca atgggagctg 840  
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gtgcaaggac acctgcccc cactcatgct ctacaacccc accacgtacc agatggatgt 1080

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ggaagacggc gtccgcaagt gtaagaagt cgaagggcct tgccgcaaag tgtgtaacgg 1260  
aataggtatt ggtgaattta aagactcact ctccataaat gctacgaata ttaaacactt 1320  
caaaaactgc acctccatca gtggcgatct ccacatcctg ccggtggcat ttagggtgga 1380  
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ttaccgttaa aaaaaaaaaa aaaaaaaaaa aaa 1593

<210> 43  
<211> 405  
<212> PRT  
<213> Homo sapiens

<400> 43  
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Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln  
20 25 30  
Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe  
35 40 45  
Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Leu Gly Asn  
50 55 60  
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys  
65 70 75 80  
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val  
85 90 95  
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr  
100 105 110  
Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn  
115 120 125  
Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu  
130 135 140  
His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu  
145 150 155 160  
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met  
165 170 175  
Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro  
180 185 190  
Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln  
195 200 205  
Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg  
210 215 220  
Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys  
225 230 235 240  
Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp  
245 250 255  
Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro  
260 265 270  
Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly  
275 280 285  
Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His  
290 295 300  
Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu  
305 310 315 320  
Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val  
325 330 335  
Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn  
340 345 350  
Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp  
355 360 365  
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr  
370 375 380  
Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu  
385 390 395 400  
Ile Thr Gly Leu Ser  
405

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<210> 44  
<211> 4473  
<212> DNA  
<213> Homo sapiens

<400> 44  
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tgggaccagg acccaccaga gcggggggct ccaccagca ccttcaaagg gacacctacg 3900  
gcagagaacc cagagtacct ggggtctggac gtgccagtgt gaaccagaag gccaaagtccg 3960  
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agtggatgcc acagcccagc ttggcccttt ccttcagat cctgggtact gaaagcctta 4260  
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<211> 1255  
<212> PRT  
<213> Homo sapiens

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20 25 30  
Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His  
35 40 45  
Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
50 55 60  
Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val  
65 70 75 80  
Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu  
85 90 95  
Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr  
100 105 110  
Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro  
115 120 125  
Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser  
130 135 140  
Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln  
145 150 155 160  
Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn  
165 170 175  
Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys  
180 185 190  
His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser  
195 200 205  
Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys  
210 215 220  
Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys  
225 230 235 240  
Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu  
245 250 255  
His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val  
260 265 270  
Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg  
275 280 285  
Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu  
290 295 300  
Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln  
305 310 315 320  
Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys  
325 330 335  
Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu  
340 345 350  
Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys  
355 360 365  
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Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
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Asp	Glu	Glu	Asp	Leu	Glu	Asp	Met	Met	Asp	Ala	Glu	Glu	Tyr	Leu	Val

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50 55 60  
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Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val  
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Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg  
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Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys  
225 230 235 240  
Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp  
245 250 255  
Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro  
260 265 270  
Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly  
275 280 285  
Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His  
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Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val  
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Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp  
355 360 365  
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr  
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180 185 190

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<213> Mus musculus

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Glu Asp Ser Thr Ser Thr Ala Val Leu Ser Gly Thr Ser Ser Pro Ala  
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Thr Thr Ala Pro Val Asn Ser Ala Ser Pro Val Ala His Gly Asp  
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Ser Thr Ser Ser Pro Val Val His Gly Gly Thr Ser Ser Pro Ala Thr  
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185 190 195  
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200 205 210  
Ser Pro Val Ala His Asp Asp Thr Ser Ser Pro Ala Thr Ser Leu Ser  
215 220 225  
Glu Asp Ser Ala Ser Ser Pro Val Ala His Gly Gly Thr Ser Ser Pro  
230 235 240  
Ala Thr Ser Pro Leu Arg Asp Ser Thr Ser Ser Pro Val His Ser Ser  
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260 265 270  
Asp His Asn Gly Thr Ser Val Thr Thr Thr Ser Ser Ala Leu Gly Ser  
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Glu Ser Val Leu Ala Thr Thr Pro Val Tyr Ser Ser Met Pro Phe Ser  
305 310 315 320  
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325 330 335  
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340 345 350  
Val Tyr Asn Thr Ser Ala Ile Ala Thr Thr Pro Val Ser Asn Gly Thr  
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Gln Pro Ser Val Pro Ser Gln Tyr Pro Val Ser Pro Thr Met Ala Thr  
370 375 380  
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420 425 430  
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500 505 510  
Glu Val Lys Val Asn Glu Met Gln Phe Pro Pro Ser Ala Gln Ser Arg  
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530 535 540  
Leu Val Ala Leu Ala Ile Val Tyr Phe Leu Ala Leu Val Cys Gln  
545 550 555 560  
Cys Arg Arg Lys Ser Tyr Gly Gln Leu Asp Ile Phe Pro Thr Gln Asp  
565 570 575  
Thr Tyr His Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg  
580 585 590  
Tyr Val Pro Pro Gly Ser Thr Lys Arg Gln Pro Tyr Glu Glu Val Ser  
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Thr Thr Ser Ala Asn Leu  
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<212> PRT  
<213> Homo sapiens

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50 55 60  
His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala  
65 70 75 80  
Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe  
85 90 95  
Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp  
100 105 110  
Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val  
115 120 125  
Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln  
130 135 140  
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<211> 1524  
<212> DNA  
<213> Homo sapiens

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<212> PRT  
<213> Homo sapiens

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50 55 60  
Gly Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp  
65 70 75 80  
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<210> 75

<211> 533

<212> PRT

<213> Mus musculus

<400> 75

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Lys Glu Cys Cys Pro Pro Trp Ile Gly Asp Gly Ser Pro Cys Gly Gln
 35      40      45
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 65      70      75      80
Pro Ser Val Phe Tyr Asn Arg Thr Cys Gln Cys Ser Gly Asn Phe Met
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Gly Phe Asn Cys Gly Asn Cys Lys Phe Gly Phe Gly Gly Pro Asn Cys
100      105      110
Thr Glu Lys Arg Val Leu Ile Arg Asn Ile Phe Asp Leu Ser Val
115      120      125
Ser Glu Lys Asn Lys Phe Phe Ser Tyr Leu Thr Leu Ala Lys His Thr
130      135      140
Ile Ser Ser Val Tyr Val Ile Pro Thr Gly Thr Tyr Gly Gln Met Asn
145      150      155      160
Asn Gly Ser Thr Pro Met Phe Asn Asp Ile Asn Ile Tyr Asp Leu Phe
165      170      175
Val Trp Met His Tyr Tyr Val Ser Arg Asp Thr Leu Leu Gly Ser
180      185      190
Glu Ile Trp Arg Gln Ile Asp Phe Ala His Glu Ala Pro Gly Phe Leu
195      200      205
Pro Trp His Arg Leu Phe Leu Leu Trp Glu Gln Glu Ile Arg Glu
210      215      220
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225      230      235      240
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Pro Glu Asn Pro Asn Leu Leu Ser Pro Ala Ser Phe Phe Ser Ser Trp
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 <213> Homo sapiens

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 Pro His Tyr Phe Pro Gln Ser Pro Pro Gln Gly Glu Asp Ser Leu Ser  
 545 550 555 560  
 Pro His Tyr Phe Pro Gln Ser Pro Pro Gln Gly Glu Asp Ser Leu Ser  
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 Pro His Tyr Phe Pro Gln Ser Pro Gln Gly Glu Asp Ser Leu Ser Pro  
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 675 680 685  
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 770 775 780  
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 785 790 795 800  
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 Phe Pro Ser Ser Thr Ser Ser Ser Leu Ser Gln Ser Ser Pro Val Ser  
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 Ser Phe Pro Ser Ser Thr Ser Ser Ser Leu Ser Lys Ser Ser Pro Glu  
 835 840 845  
 Ser Pro Leu Gln Ser Pro Val Ile Ser Phe Ser Ser Ser Thr Ser Leu  
 850 855 860  
 Ser Pro Phe Ser Glu Glu Ser Ser Ser Pro Val Asp Glu Tyr Thr Ser  
 865 870 875 880  
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 Tyr Phe Pro Val Ile Phe Arg Lys Ala Arg Glu Phe Ile Glu Ile Leu  
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gtgggtggcaa cagagatggc agcgagctg gagtggttagg agggcggcct gagcggtagg 180  
agtggggctg gagcagtaag atggcggcca gagcggtttt tctggcattg tctgcccagc 240  
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aagacggcac agctctgtgc ttcattcttct gaggttgtgg cagccacggg gatggagacg 360  
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gatctcctga cctcgtgatc cgcccgcctt ggctttccaa agtgccgaga ttacagcgat 480  
gtgcattttg taagcacttt ggagccacta tcaaattgctg tgaagagaaa tgtacccaga 540  
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<212> PRT  
<213> Homo sapiens

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Pro Glu Asp Gly Thr Ala Leu Cys Phe Ile Phe  
35 40

<210> 82  
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35 40 45
Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala Ser
50 55 60
Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly His
65 70 75 80
Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu Met
85 90 95
Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Glu Met Arg
100 105 110
Ser His Tyr Val Ala Gln Thr Gly Ile Leu Trp Leu Leu Met Asn Asn
115 120 125
Cys Phe Leu Asn Leu Ser Pro Arg Lys Pro
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<213> Homo sapiens
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gagaaaacag ctggtgattt atgaagagat cagcgaccct gaggaagatg acgagtaact 660
cccctcaggg atacgacaca tgcccattgat gagaagcaga acgtggtgac ctttcacgaa 720
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<212> PRT
<213> Homo sapiens
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 Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg  
           85                  90                  95  
 Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met  
           100                 105                 110  
 Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu  
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 Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys  
           130                 135                 140  
 Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly  
           145                 150                 155                 160  
 Glu His Ala Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile  
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 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly  
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 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile  
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 115 120 125  
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 180 185 190  
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<210> 89  
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<212> PRT

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<213> Homo sapiens

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Ala Tyr Lys Gln Gln Ser Leu Leu His Pro Asp Lys Gly Gly Ser
 35      40      45
His Ala Leu Met Gln Glu Leu Asn Ser Leu Trp Gly Thr Phe Lys Thr
 50      55      60
Glu Val Tyr Asn Leu Arg Met Asn Leu Gly Gly Thr Gly Phe Gln Gly
 65      70      75      80
Ser Pro Pro Arg Thr Ala Glu Arg Gly Thr Glu Glu Ser Gly His Ser
 85      90      95
Pro Leu His Asp Asp Tyr Trp Ser Phe Ser Tyr Gly Ser Lys Tyr Phe
100      105      110
Thr Arg Glu Trp Asn Asp Phe Phe Arg Lys Trp Asp Pro Ser Tyr Gln
115      120      125
Ser Pro Pro Lys Thr Ala Glu Ser Ser Glu Gln Pro Asp Leu Phe Cys
130      135      140
Tyr Glu Glu Pro Leu Leu Ser Pro Asn Pro Ser Ser Pro Thr Asp Thr
145      150      155      160
Pro Ala His Thr Ala Gly Arg Arg Arg Asn Pro Cys Val Ala Glu Pro
165      170      175
Asp Asp Ser Ile Ser Pro Asp Pro Pro Arg Thr Pro Val Ser Arg Lys
180      185      190      195
Arg Pro Arg Pro Ala Gly Ala Thr Gly Gly Gly Gly Gly Val His
195      200      205      210
Ala Asn Gly Gly Ser Val Phe Gly His Pro Thr Gly Gly Thr Ser Thr
210      215      220      225
Pro Ala His Pro Pro Pro Tyr His Ser Gln Gly Gly Ser Glu Ser Met
225      230      235      240
Gly Gly Ser Asp Ser Ser Gly Phe Ala Glu Gly Ser Phe Arg Ser Asp
245      250      255
Pro Arg Cys Glu Ser Glu Asn Glu Ser Tyr Ser Gln Ser Cys Ser Gln
260      265      270      275
Ser Ser Phe Asn Ala Thr Pro Pro Lys Lys Ala Arg Glu Asp Pro Ala
275      280      285      290
Pro Ser Asp Phe Pro Ser Ser Leu Thr Gly Tyr Leu Ser His Ala Ile
290      295      300      305
Tyr Ser Asn Lys Thr Phe Pro Ala Phe Leu Val Tyr Ser Thr Lys Glu
305      310      315      320
Lys Cys Lys Gln Leu Tyr Asp Thr Ile Gly Lys Phe Arg Pro Glu Phe
325      330      335      340
Lys Cys Leu Val His Tyr Glu Glu Gly Gly Met Leu Phe Phe Leu Thr
340      345      350      355
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355      360      365      370
Cys Ser Val Ser Phe Leu Met Cys Lys Ala Val Thr Lys Pro Met Glu
370      375      380      385
Cys Tyr Gln Val Val Thr Ala Ala Pro Phe Gln Leu Ile Thr Glu Asn
385      390      395      400
Lys Pro Gly Leu His Gln Phe Glu Phe Thr Asp Glu Pro Glu Glu Gln
405      410      415      420
Lys Ala Val Asp Trp Ile Met Val Ala Asp Phe Ala Leu Glu Asn Asn
420      425      430      435
Leu Asp Asp Pro Leu Leu Ile Met Gly Tyr Tyr Leu Asp Phe Ala Lys
435      440      445      450
Glu Val Pro Ser Cys Ile Lys Cys Ser Lys Glu Glu Thr Arg Leu Gln
450      455      460      465
Ile His Trp Lys Asn His Arg Lys His Ala Glu Asn Ala Asp Leu Phe
465      470      475      480
Leu Asn Cys Lys Ala Gln Lys Thr Ile Cys Gln Gln Ala Ala Asp Gly
485      490      495      500
Val Leu Ala Ser Arg Arg Leu Lys Leu Val Glu Cys Thr Arg Ser Gln
500      505      510      515
Leu Leu Lys Glu Arg Leu Gln Gln Ser Leu Leu Arg Leu Lys Glu Leu
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                           565                          570                          575  
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                           580                          585                          590  
 Gly Gly Lys Ser Leu Asn Ile Asn Cys Pro Ala Asp Lys Leu Ala Phe  
           595                          600                          605  
 Glu Leu Gly Val Ala Gln Asp Gln Phe Val Val Cys Phe Glu Asp Val  
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 Lys Gly Gln Ile Ala Leu Asn Lys Gln Leu Gln Pro Gly Met Gly Val  
           625                          630                          635                          640  
 Ala Asn Leu Asp Asn Leu Arg Asp Tyr Leu Asp Gly Ser Val Lys Val  
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 Asn Leu Glu Lys Lys His Ser Asn Lys Arg Ser Gln Leu Phe Pro Pro  
           660                          665                          670  
 Cys Val Cys Thr Met Asn Glu Tyr Leu Leu Pro Gln Thr Val Trp Ala  
           675                          680                          685  
 Arg Phe His Met Val Leu Asp Phe Thr Cys Lys Pro His Leu Ala Gln  
           690                          695                          700  
 Ser Leu Glu Lys Cys Glu Phe Leu Gln Arg Glu Arg Ile Ile Gln Ser  
           705                          710                          715                          720  
 Gly Asp Thr Leu Ala Leu Leu Leu Ile Trp Asn Phe Thr Ser Asp Val  
                           725                          730                          735  
 Phe Asp Pro Asp Ile Gln Gly Leu Val Lys Glu Val Arg Asp Gln Phe  
           740                          745                          750  
 Ala Ser Glu Cys Ser Tyr Ser Leu Phe Cys Asp Ile Leu Cys Asn Val  
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<210> 91  
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<212> PRT

<213> Homo sapiens

<400> 91

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 35      40      45
Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
 50      55      60
Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
 65      70      75      80
Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
 85      90      95
Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
 100      105      110
Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
 115      120      125
Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
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Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
 145      150      155      160
Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
 165      170      175
Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
 180      185      190
Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
 195      200      205
Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
 210      215      220
Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
 225      230      235      240
Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
 245      250      255
Ala Thr Glu Glu Arg Gly Arg Lys Pro Gln Gln Ile Pro Ala Ser Thr
 260      265      270
Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His
 275      280      285
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Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
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<211> 2026

<212> DNA

<213> Homo sapiens

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<210> 93  
<211> 495  
<212> PRT  
<213> Homo sapiens

<400> 93

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			20					25					30		
Phe	Gln	Ala	Arg	Leu	Thr	Arg	Ser	Asn	Ser	Lys	Cys	Gln	Gly	Gln	Leu
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65				70				75						80	
Cys	Gln	Arg	Leu	Asn	Cys	Gly	Val	Pro	Leu	Ser	Leu	Gly	Pro	Phe	Leu
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Val	Thr	Tyr	Thr	Pro	Gln	Ser	Ser	Ile	Ile	Cys	Tyr	Gly	Gln	Leu	Gly
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Ser	Phe	Ser	Asn	Cys	Ser	His	Ser	Arg	Asn	Asp	Met	Cys	His	Ser	Leu
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Pro	Pro	Pro	Thr	Thr	Thr	Pro	Glu	Pro	Thr	Ala	Pro	Pro	Arg	Leu	Gln
145				150						155				160	
Leu	Val	Ala	Gln	Ser	Gly	Gly	Gln	His	Cys	Ala	Gly	Val	Val	Glu	Phe
			165					170						175	
Tyr	Ser	Gly	Ser	Leu	Gly	Gly	Thr	Ile	Ser	Tyr	Glu	Ala	Gln	Asp	Lys
	180						185						190		
Thr	Gln	Asp	Leu	Glu	Asn	Phe	Leu	Cys	Asn	Asn	Leu	Gln	Cys	Gly	Ser
	195					200					205				
Phe	Leu	Lys	His	Leu	Pro	Glu	Thr	Glu	Ala	Gly	Arg	Ala	Gln	Asp	Pro
	210				215						220				
Gly	Glu	Pro	Arg	Glu	His	Gln	Pro	Leu	Pro	Ile	Gln	Trp	Lys	Ile	Gln
225				230						235				240	
Asn	Ser	Ser	Cys	Thr	Ser	Leu	Glu	His	Cys	Phe	Arg	Lys	Ile	Lys	Pro
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Gln	Lys	Ser	Gly	Arg	Val	Leu	Ala	Leu	Leu	Cys	Ser	Gly	Phe	Gln	Pro
			260				265						270		
Lys	Val	Gln	Ser	Arg	Leu	Val	Gly	Ser	Ser	Ile	Cys	Glu	Gly	Thr	
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Val	Glu	Val	Arg	Gln	Gly	Ala	Gln	Trp	Ala	Ala	Leu	Cys	Asp	Ser	Ser
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Ser	Ala	Arg	Ser	Ser	Leu	Arg	Trp	Glu	Glu	Val	Cys	Arg	Glu	Gln	Gln
305				310						315				320	
Cys	Gly	Ser	Val	Asn	Ser	Tyr	Arg	Val	Leu	Asp	Ala	Gly	Asp	Pro	Thr

WO 2005/037989

PCT/US2003/024918

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 Asp Pro Asn Pro Ala Gly Leu Ala Ala Gly Thr Val Ala Ser Ile Ile  
 370 375 380  
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 385 390 395 400  
 Ala Tyr Lys Lys Leu Val Lys Lys Phe Arg Gln Lys Lys Gln Arg Gln  
 405 410 415  
 Trp Ile Gly Pro Thr Gly Met Asn Gln Asn Met Ser Phe His Arg Asn  
 420 425 430  
 His Thr Ala Thr Val Arg Ser His Ala Glu Asn Pro Thr Ala Ser His  
 435 440 445  
 Val Asp Asn Glu Tyr Ser Gln Pro Pro Arg Asn Ser Arg Leu Ser Ala  
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 Asn Ser Ser Asp Ser Asp Tyr Asp Leu His Gly Ala Gln Arg Leu  
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 <213> Homo sapiens

<400> 94  
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 tctcttcact attttggat tgtgcaagtc atcttacctc tctggatctc agttgtctca 180  
 tctgtaaaaa ggagataaaa attatttacc tgcctgaaca tgagggtggag gaccatcctg 240  
 ctacagtatt gctttctctt gattacatgt ttacttactg ctcttgaagc tgtgcctatt 300  
 gacatagaca agacaaaagt acaaaatatt caccctgtgg aaagtgcgaa gatagaacca 360  
 ccagatactg gactttatta tgatgaatat ctcaagcaag tgattgatgt gctggaaaaca 420  
 gataaacact tcagagaaaa gctccagaaa gcagacatag aggaaataaa gagtgggagg 480  
 ctaagcaaaag aactggattt agtaagtcac catgtgagga caaaacttga tgaactgaaa 540  
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 ataggcatgg accaccaagc tcttctaaaa caatttgatc acctaaacca cctgaatcct 660  
 gacaagtgtg aatccacaga tttagatatg ctaatcaaag cggcaacaag tgatctggaa 720  
 cactatgaca agactcgtca tgaagaatgt aaaaaatatg aaatgatgaa ggaacatgaa 780  
 aggagagaat atttaaaaac attgaatgaa gaaaagagaa aagaagaaga gtctaaattt 840  
 gaagaaatga agaaaaagca tgaaaatcac cctaaagtta atcaccagg aagcaaaaga 900  
 caactaaaag aggtatggga agagactgat ggattggatc ctaatgactt tgaccccaag 960  
 acatttttca aattacatga tgtcaatagt gatggattcc tggatgaaca agaattagaa 1020  
 gccctattta ctaaaaggtt ggagaaaagta tatgacccta aaaatgaaga ggatgatatg 1080  
 gtagaatgg aagaagaaag gcttagaatg agggaaatg taatgaatga ggttgatact 1140  
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 ttggagccag atagctggga gacattagat cagcaacagt tcttcacaga ggaagaacta 1260  
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 cttcagaaaac aaaaagaaga gctacaacgt cagcatgatc aactggaggc tcagaagctg 1380  
 gaatatcatc aggtcataca gcagatggaa caaaaaaat tacaacaagg aattcctcca 1440  
 tcagggccag ctggagaatt gaagtttgag ccacacattt aaagtctgaa gtccaccaga 1500  
 acttggaaaga aagctgttaa ctcaacatct atttcatctt tttagctccc ttcccttttc 1560  
 tctgctcaat aaatatatta aaagca 1586

<210> 95  
 <211> 420  
 <212> PRT  
 <213> Homo sapiens

<400> 95  
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 Cys Leu Leu Thr Ala Leu Glu Ala Val Pro Ile Asp Ile Asp Lys Thr  
 20 25 30  
 Lys Val Gln Asn Ile His Pro Val Glu Ser Ala Lys Ile Glu Pro Pro  
 35 40 45

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 50 55 60  
 Leu Glu Thr Asp Lys His Phe Arg Glu Lys Leu Gln Lys Ala Asp Ile  
 65 70 75 80  
 Glu Glu Ile Lys Ser Gly Arg Leu Ser Lys Glu Leu Asp Leu Val Ser  
 85 90 95  
 His His Val Arg Thr Lys Leu Asp Glu Leu Lys Arg Gln Glu Val Gly  
 100 105 110  
 Arg Leu Arg Met Leu Ile Lys Ala Lys Leu Asp Ser Leu Gln Asp Ile  
 115 120 125  
 Gly Met Asp His Gln Ala Leu Leu Lys Gln Phe Asp His Leu Asn His  
 130 135 140  
 Leu Asn Pro Asp Lys Phe Glu Ser Thr Asp Leu Asp Met Leu Ile Lys  
 145 150 155 160  
 Ala Ala Thr Ser Asp Leu Glu His Tyr Asp Lys Thr Arg His Glu Glu  
 165 170 175  
 Phe Lys Lys Tyr Glu Met Met Lys Glu His Glu Arg Arg Glu Tyr Leu  
 180 185 190  
 Lys Thr Leu Asn Glu Glu Lys Arg Lys Glu Glu Glu Ser Lys Phe Glu  
 195 200 205  
 Glu Met Lys Lys Lys His Glu Asn His Pro Lys Val Asn His Pro Gly  
 210 215 220  
 Ser Lys Asp Gln Leu Lys Glu Val Trp Glu Glu Thr Asp Gly Leu Asp  
 225 230 235 240  
 Pro Asn Asp Phe Asp Pro Lys Thr Phe Phe Lys Leu His Asp Val Asn  
 245 250 255  
 Ser Asp Gly Phe Leu Asp Glu Gln Glu Leu Glu Ala Leu Phe Thr Lys  
 260 265 270  
 Glu Leu Glu Lys Val Tyr Asp Pro Lys Asn Glu Glu Asp Asp Met Val  
 275 280 285  
 Glu Met Glu Glu Glu Arg Leu Arg Met Arg Glu His Val Met Asn Glu  
 290 295 300  
 Val Asp Thr Asn Lys Asp Arg Leu Val Thr Leu Glu Glu Phe Leu Lys  
 305 310 315 320  
 Ala Thr Glu Lys Lys Glu Phe Leu Glu Pro Asp Ser Trp Glu Thr Leu  
 325 330 335  
 Asp Gln Gln Gln Phe Phe Thr Glu Glu Glu Leu Lys Glu Tyr Glu Asn  
 340 345 350  
 Ile Ile Ala Leu Gln Glu Asn Glu Leu Lys Lys Lys Ala Asp Glu Leu  
 355 360 365  
 Gln Lys Gln Lys Glu Glu Leu Gln Arg Gln His Asp Gln Leu Glu Ala  
 370 375 380  
 Gln Lys Leu Glu Tyr His Gln Val Ile Gln Gln Met Glu Gln Lys Lys  
 385 390 395 400  
 Leu Gln Gln Gly Ile Pro Pro Ser Gly Pro Ala Gly Glu Leu Lys Phe  
 405 410 415  
 Glu Pro His Ile  
 420

<210> 96  
 <211> 1204  
 <212> DNA  
 <213> Homo sapiens

<400> 96  
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 gtggctgtgc gttctgggga ccttggtggg gctctcagct actccagccc ccaagagctg 180  
 cccagagagg cactactggg ctccaggaaa gctgtgctgc cagatgtgtg agccaggaaac 240  
 attcctcgtg aaggactgtg accagcatag aaaggctgct cagtgtgata cttgcataacc 300  
 gggggtctcc ttctctcctg accaccacac ccggcccccac tgtgagagct gtcggcactg 360  
 taactctggt cttctcgttc gcaactgcac catcactgcc aatgctgagt gtgctgtctg 420  
 caatggctgg cagtgcaggg acaaggagtg caccgagtgt gatcctcttc caaaccttc 480  
 gctgaccgct cggctcgttc aggcctgag cccacaccct cagcccaccc acttacctta 540  
 tgtcagttag atgctggagg ccaggacagc tgggcacatg cagactctgg ctgacttcag 600  
 gcagctgcct gcccggaact tctctaccca ctggccaccc caaagatccc tgtgcagctc 660  
 cgatctttatt cgcatccttg tgatcttctc tggaatgttc cttgttttca ccctggccgg 720  
 ggccctgttc ctccatcaac gaaggaaata tagatcaaac aaaggagaaa gtcctgtgga 780



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ctgcactaca gccctggcct ccacccccac cccgccgacc atccaaggga gaggtagacc 960  
tggcagccac aactgcagtc ccacccctctt gtcaggggccc ttctctgtgt acacgtgaca 1020  
gagtgccctt tcgagactgg cagggacgag gacaaatat gatgaggttg agagtgggaa 1080  
gcaggagccc agccagctgc gcctgcgctg caggagggcg ggggctcttg ttgtaaaaca 1140  
cacttcctgc tgcgaaagac ccacatgcta caagacgggc aaaataaagt gacagatgac 1200  
cacc 1204

<210> 97  
<211> 260  
<212> PRT  
<213> Homo sapiens

<400> 97  
Met Ala Arg Pro His Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val  
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Gly Leu Ser Ala Thr Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr  
20 25 30  
Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe  
35 40 45  
Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro  
50 55 60  
Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His  
65 70 75 80  
Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys  
85 90 95  
Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys  
100 105 110  
Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu  
115 120 125  
Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His  
130 135 140  
Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met  
145 150 155 160  
Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr  
165 170 175  
His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile  
180 185 190  
Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala  
195 200 205  
Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser  
210 215 220  
Pro Val Glu Pro Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu  
225 230 235 240  
Glu Gly Ser Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro  
245 250 255  
Ala Cys Ser Pro  
260

<210> 98  
<211> 1514  
<212> DNA  
<213> Homo sapiens

<400> 98  
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gaggaggggc tggaacccta gccatcgctc aggacaaaga tgctcaggct gctcttggtt 120  
ctcaacttat tcccttcaat tcaagtaaca ggaaacaaga ttttggtgaa gcagtcgccc 180  
atgctttag cgtacgacaa tgcggtcaac cttagctgca agtattccta caatctcttc 240  
tcaaggagat tccgggcatc ccttcacaaa ggactggata gtgctgtgga agtctgtgtt 300  
gtatatggga attactccca gcagcttcag gtttactcaa aaacggggtt caactgtgat 360  
gggaaattgg gcaatgaatc agtgacattc tacctccaga atttgatgt taaccaaaca 420  
gatatttact tctgcaaaat tgaagttag tctcctctc cttacctaga caatgagaag 480  
agcaatggaa ccattatcca tgtgaaagg aaacaccttt gtccaagtcc cctatttccc 540  
ggacatttcta agcccttttg ggtgctgggt gtggttggtg gagtcctggc ttgctatagc 600  
ttgctagtaa cagtggcctt tattatttct tgggtgagga gtaagaggag caggctcctg 660  
cacagtgact acatgaacat gactccccgc cgccccgggc ccaccgcaa gcattaccag 720

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 ccatctccag cgggccacct cagccctgtg tgggccacca atgccaattt ttctcgagtg 900  
 actagaccaa atatcaagat cattttgaga ctctgaaatg aagtaaaaga gatttcctgt 960  
 gacaggccaa gtcttacagt gccatggccc acattccaac ttaccatgta cttagtgtact 1020  
 tgactgagaa gttagggttag aaaacaaaaa gggagtggat tctgggagcc tcttcccttt 1080  
 ctactcacc tgcacatctc agtcaagcaa agtgtggtat ccacagacat tttagttgca 1140  
 gaagaaaggc taggaaatca ttccttttgg tttaaagggt gtttaacttt ttgggttagtg 1200  
 ggtaaacgg ggtaagttag agtaggggga gggataggaa gacatattta aaaaccatta 1260  
 aaacactgtc tcccactcat gaaatgagcc acgtagtctc tatttaatgc tgttttcctt 1320  
 tagtttagaa atacatagac attgtctttt atgaattctg atcatattta gtcattttga 1380  
 ccaaatgagg gatttggtca aatgagggat tccctcaaag caatatcagg taaaccaagt 1440  
 tgctttcctc actccctgtc atgagacttc agtggttaatg ttcacaatat actttcgaaa 1500  
 gaataaaata gttc 1514

<210> 99  
 <211> 220  
 <212> PRT  
 <213> Homo sapiens

<400> 99  
 Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val  
 1 5 10 15  
 Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr  
 20 25 30  
 Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser  
 35 40 45  
 Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu  
 50 55 60  
 Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser  
 65 70 75 80  
 Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr  
 85 90 95  
 Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys  
 100 105 110  
 Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser  
 115 120 125  
 Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro  
 130 135 140  
 Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly  
 145 150 155 160  
 Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile  
 165 170 175  
 Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met  
 180 185 190  
 Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro  
 195 200 205  
 Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser  
 210 215 220

<210> 100  
 <211> 672  
 <212> DNA  
 <213> Homo sapiens

<400> 100  
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 ccttgcactc tctgtttttt tcttctcttc atccctgtct tctgcaaagc aatgcacgtg 120  
 gccagcctg ctgtgttact ggccagcagc cgaggcatcg ccagctttgt gtgtgagtat 180  
 gcatctccag gcaaagccac tgaggtccgg gtgacagtgc ttcggcaggc tgacagccag 240  
 gtgactgaag tctgtgcggc aacctacatg acggggaatg agttgacctt cctagatgat 300  
 tccatctgca cgggcacctc cagtggaaat caagtgaacc tcactatcca aggactgagg 360  
 gccatggaca cgggactcta catctgcaag gtggagctca tgtaccacc gccatactac 420  
 ctgggcatag gcaacggaac ccagatttat gtaattgatc cagaaccgtg ccagatttct 480  
 gacttctcc tctggatcct tgcagcagtt agttcggggt tgttttttta tagctttctc 540  
 ctcacagctg tttcttttag caaaatgcta aagaaaagaa gccctcttac aacaggggtc 600  
 tatgtgaaaa tgccccaac agagccagaa tgtgaaaagc aatttcagcc ttattttatt 660  
 cccatcaatt ga 672

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<210> 101  
<211> 223  
<212> PRT  
<213> Homo sapiens

<400> 101  
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20 25 30  
Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala  
35 40 45  
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly  
50 55 60  
Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln  
65 70 75 80  
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr  
85 90 95  
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val  
100 105 110  
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile  
115 120 125  
Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly  
130 135 140  
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
145 150 155 160  
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
165 170 175  
Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
180 185 190  
Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
195 200 205  
Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn  
210 215 220

<210> 102  
<211> 2339  
<212> DNA  
<213> Homo sapiens

<400> 102  
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gaaaatgagg cccaaagaag tgaatgccact tgggttaaggt cccagagcag gtcagaatca 120  
gacctaggat cagaaacctg gctcctggct cctgctccct actcttctaa ggatcgctgt 180  
cctgacagaa gagaactcct ctttcctaaa atggagtcga gtaaaaagat ggactctcct 240  
ggcgcgctgc agactaaccg gccgctaaag ctgcacactg accgcagtgc tgggacgccca 300  
gtttttgtcc ctgaacaagg aggttacaag gaaaagtgtg tgaagaccgt ggaggacaag 360  
tacaagtgtg agaagtgccca cctgggtgctg tgcagcccga agcagaccga gtgtgggcac 420  
cgcttctgcg agagctgcat ggcgccctg ctgagctctt caagtccaaa atgtacagcg 480  
tgtcaagaga gcatcgttaa agataagggtg ttttaaggata attgctgcaa gagagaaatt 540  
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taccgggaag ccacatgcag ccactgcaag cagatggttc cgatgactgc gctgcgtaaa 780  
cacgaagaca ccgactgtcc ctgctgtggtg gtgtcctgcc ctcaacaagt cagcgtccag 840  
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tgtagtttta agcgctatgg ctgctgtttt caggggacaa accagcagat caaggcccac 960  
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aatgaatcca aaatccttca ttacacgca gtgatagaca gccaagcaga gaaactgaag 1200  
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agcagcgtgg agtccctcca gaaccgcgtg accgagctgg agagcgtgga caagagcgcg 1320  
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ctgagtgtgc acgacatccg cctagccgac atggacctgg gcttccaggt cctggagacc 1440  
gccagctaca atggagtgtc catctggaag attcgcgact acaagcggcg gaagcaggag 1500  
gccgtcatgg ggaagaccct gtccctttac agccagcctt tctacactgg ttactttggc 1560

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 gatacaattt ttattaaagt catagtggat acttcggatc tgcccgatcc ctgataagta 1920  
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 ccacacttca ctctgaagaa ttatttatcc ttcaacaaga taaatattgc tgtcagagaa 2160  
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 acgtggggat agctggacat gtcagcatgt taagtaaaag gagaatttat gaaatagta 2339

<210> 103  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 103  
 Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn  
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 Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe  
 20 25 30  
 Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu  
 35 40 45  
 Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys  
 50 55 60  
 Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu  
 65 70 75 80  
 Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val  
 85 90 95  
 Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala  
 100 105 110  
 Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu  
 115 120 125  
 Met Leu Gly His Leu Val His Leu Lys Asn Asp Cys His Phe Glu Glu  
 130 135 140  
 Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys Asp  
 145 150 155 160  
 Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys  
 165 170 175  
 Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His Glu  
 180 185 190  
 Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser  
 195 200 205  
 Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys  
 210 215 220  
 Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe  
 225 230 235 240  
 Gln Gly Thr Asn Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val  
 245 250 255  
 Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys  
 260 265 270  
 Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln  
 275 280 285  
 Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln  
 290 295 300  
 Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg  
 305 310 315 320  
 Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile  
 325 330 335  
 Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser  
 340 345 350  
 Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys  
 355 360 365  
 Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu  
 370 375 380  
 Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala Asp

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 385 390 395 400  
 Met Asp Leu Gly Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val  
 405 410 415  
 Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val  
 420 425 430  
 Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr  
 435 440 445  
 Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met  
 450 455 460  
 Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu  
 465 470 475 480  
 Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met  
 485 490 495  
 Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys  
 500 505 510  
 Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn  
 515 520 525  
 Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn  
 530 535 540  
 Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp  
 545 550 555 560  
 Thr Ser Asp Leu Pro Asp Pro  
 565

<210> 104  
 <211> 1874  
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 <213> Homo sapiens

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 ggactgtgat ggtcaacctg aacatccata accggaatac caataccaat cccaaaagg 240  
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 gaaggaagg tttgactgagt accaatttgc ttcttgttta cttttttaag ggctttaagt 780  
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 <213> Homo sapiens

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Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn  
35 40 45  
Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser  
50 55 60  
Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu  
65 70 75 80  
Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His  
85 90 95  
Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser  
100 105 110  
Val Pro Ile Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His  
115 120 125  
Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys  
130 135 140  
Thr Cys Val Thr Pro Ile Val His His Val Ala  
145 150 155

<210> 106  
<211> 3120  
<212> DNA  
<213> Homo sapiens

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tgaaggtaac cagcccaatg atgagctcag acagcctgtg ggaccccaac atcacctgtg 660  
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 agaactcggg ctgggacacg atggggtcag agtcagaggg gcccatgtga tgaggcggc 2640  
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<210> 107  
 <211> 866  
 <212> PRT  
 <213> Homo sapiens

<400> 107  
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 20 25 30  
 Leu Arg Leu Leu Asp His Arg Ala Leu Val Cys Ser Gln Pro Gly Leu  
 35 40 45  
 Asn Cys Thr Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His  
 50 55 60  
 Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp Leu Gln Ile Gln Leu  
 65 70 75 80  
 His Phe Ala His Thr Gln Gln Gly Asp Leu Phe Pro Val Ala His Ile  
 85 90 95  
 Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala  
 100 105 110  
 Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Arg  
 115 120 125  
 Phe Glu Phe Leu Ser Lys Leu Arg His His His Arg Arg Trp Arg Phe  
 130 135 140  
 Thr Phe Ser His Phe Val Val Asp Pro Asp Gln Tyr Glu Val Thr  
 145 150 155 160  
 Val His His Leu Pro Lys Pro Ile Pro Asp Gly Asp Pro Asn His Gln  
 165 170 175  
 Ser Lys Asn Phe Leu Val Pro Asp Cys Glu His Ala Arg Met Lys Val  
 180 185 190  
 Thr Thr Pro Cys Met Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr  
 195 200 205  
 Val Glu Thr Leu Glu Ala His Gln Leu Arg Val Ser Phe Thr Leu Trp  
 210 215 220  
 Asn Glu Ser Thr His Tyr Gln Ile Leu Leu Thr Ser Phe Pro His Met  
 225 230 235 240  
 Glu Asn His Ser Cys Phe Glu His Met His Ile Pro Ala Pro Arg  
 245 250 255  
 Pro Glu Glu Phe His Gln Arg Ser Asn Val Thr Leu Thr Leu Arg Asn  
 260 265 270  
 Leu Lys Gly Cys Cys Arg His Gln Val Gln Ile Gln Pro Phe Phe Ser  
 275 280 285  
 Ser Cys Leu Asn Asp Cys Leu Arg His Ser Ala Thr Val Ser Cys Pro  
 290 295 300  
 Glu Met Pro Asp Thr Pro Glu Pro Ile Pro Asp Tyr Met Pro Leu Trp  
 305 310 315 320  
 Val Tyr Trp Phe Ile Thr Gly Ile Ser Ile Leu Leu Val Gly Ser Val  
 325 330 335  
 Ile Leu Leu Ile Val Cys Met Thr Trp Arg Leu Ala Gly Pro Gly Ser  
 340 345 350  
 Glu Lys Tyr Ser Asp Asp Thr Lys Tyr Thr Asp Gly Leu Pro Ala Ala  
 355 360 365  
 Asp Leu Ile Pro Pro Pro Leu Lys Pro Arg Lys Val Trp Ile Ile Tyr  
 370 375 380  
 Ser Ala Asp His Pro Leu Tyr Val Asp Val Val Leu Lys Phe Ala Gln

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 420 425 430  
 Lys Gln Glu Met Val Glu Ser Asn Ser Lys Ile Ile Val Leu Cys Ser  
 435 440 445  
 Arg Gly Thr Arg Ala Lys Trp Gln Ala Leu Leu Gly Arg Gly Ala Pro  
 450 455 460  
 Val Arg Leu Arg Cys Asp His Gly Lys Pro Val Gly Asp Leu Phe Thr  
 465 470 475 480  
 Ala Ala Met Asn Met Ile Leu Pro Asp Phe Lys Arg Pro Ala Cys Phe  
 485 490 495  
 Gly Thr Tyr Val Val Cys Tyr Phe Ser Glu Val Ser Cys Asp Gly Asp  
 500 505 510  
 Val Pro Asp Leu Phe Gly Ala Ala Pro Arg Tyr Pro Leu Met Asp Arg  
 515 520 525  
 Phe Glu Glu Val Tyr Phe Arg Ile Gln Asp Leu Glu Met Phe Gln Pro  
 530 535 540  
 Gly Arg Met His Arg Val Gly Glu Leu Ser Gly Asp Asn Tyr Leu Arg  
 545 550 555 560  
 Ser Pro Gly Gly Arg Gln Leu Arg Ala Ala Leu Asp Arg Phe Arg Asp  
 565 570 575  
 Trp Gln Val Arg Cys Pro Asp Trp Phe Glu Cys Glu Asn Leu Tyr Ser  
 580 585 590  
 Ala Asp Asp Gln Asp Ala Pro Ser Leu Asp Glu Glu Val Phe Glu Glu  
 595 600 605  
 Pro Leu Leu Pro Pro Gly Thr Ile Val Lys Arg Ala Pro Leu Val  
 610 615 620  
 Arg Glu Pro Gly Ser Gln Ala Cys Leu Ala Ile Asp Pro Leu Val Gly  
 625 630 635 640  
 Glu Glu Gly Gly Ala Val Ala Lys Leu Glu Pro His Leu Gln Pro  
 645 650 655  
 Arg Gly Gln Pro Ala Pro Gln Pro Leu His Thr Leu Val Leu Ala Ala  
 660 665 670  
 Glu Glu Gly Ala Leu Val Ala Ala Val Glu Pro Gly Pro Ala Asp  
 675 680 685  
 Gly Ala Ala Val Arg Leu Ala Leu Ala Gly Glu Gly Glu Ala Cys Pro  
 690 695 700  
 Leu Leu Gly Ser Pro Gly Ala Gly Arg Asn Ser Val Leu Phe Leu Pro  
 705 710 715 720  
 Val Asp Pro Glu Asp Ser Pro Leu Gly Ser Ser Thr Pro Met Ala Ser  
 725 730 735 740  
 Pro Asp Leu Leu Pro Glu Asp Val Arg Glu His Leu Glu Gly Leu Met  
 745 750 755  
 Leu Ser Leu Phe Glu Gln Ser Leu Ser Cys Gln Ala Gln Gly Gly Cys  
 760 765 770  
 Ser Arg Pro Ala Met Val Leu Thr Asp Pro His Thr Pro Tyr Glu Glu  
 775 780 785  
 Glu Gln Arg Gln Ser Val Gln Ser Asp Gln Gly Tyr Ile Ser Arg Ser  
 790 795 800  
 Ser Pro Gln Pro Pro Gly Leu Thr Glu Met Glu Glu Glu Glu Glu  
 805 810 815  
 Glu Glu Gln Asp Pro Gly Lys Pro Ala Leu Pro Leu Ser Pro Glu Asp  
 820 825 830  
 Leu Glu Ser Leu Arg Ser Leu Gln Arg Gln Leu Leu Phe Arg Gln Leu  
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<210> 108  
 <211> 578  
 <212> DNA  
 <213> Homo sapiens  
 <400> 108



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 gccattcagg tcatagcctg cagtgtctaca actgtcctaa cccaactgct gactgcaaaa 180  
 cagccgtcaa ttgttcatct gattttgatg cgtgtctcat taccaaagct gggttacaag 240  
 tgtataacaa gtgttggaag tttagcatt gcaatttcaa cgacgtcaca acccgcttga 300  
 gggaaaatga gctaacgtac tactgtgca agaaggacct gtgtaacttt aacgaacagc 360  
 ttgaaaatgg tgggacatcc ttatcagaga aaacagttct tctgtgtgtg actccatttc 420  
 tggcagcagc ctggagcctt catccctaag tcaacaccag gagagcttct cccaaactcc 480  
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 atggatcctg ttgggaaaga ataaaattag cttgagca 578

<210> 109  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 109  
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 20 25 30  
 Asn Pro Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe  
 35 40 45  
 Asp Ala Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys  
 50 55 60  
 Trp Lys Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg  
 65 70 75 80  
 Glu Asn Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe  
 85 90 95  
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 100 105 110  
 Leu Leu Leu Val Thr Pro Phe Leu Ala Ala Ala Trp Ser Leu His Pro  
 115 120 125

<210> 110  
 <211> 1048  
 <212> DNA  
 <213> Homo sapiens

<400> 110  
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 tggctctccg cagcaacgtg actctgaaca tctctgagag cctgcctgag aactacaaac 180  
 aactaacctg gttttatact ttcgaccaga agattgtaga atgggattcc agaaaatcta 240  
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 gggtattatt taattttata tccctttgtt gttttgtagt acacagagat tatagagata 960  
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 taaaaagata taattataaa aaaaaaaa 1048

<210> 111  
 <211> 243  
 <212> PRT  
 <213> Homo sapiens

<400> 111  
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 35 40 45  
 Leu Pro Glu Asn Tyr Lys Gln Leu Thr Trp Phe Tyr Thr Phe Asp Gln  
 50 55 60  
 Lys Ile Val Glu Trp Asp Ser Arg Lys Ser Lys Tyr Phe Glu Ser Lys  
 65 70 75 80  
 Phe Lys Gly Arg Val Arg Leu Asp Pro Gln Ser Gly Ala Leu Tyr Ile  
 85 90 95  
 Ser Lys Val Gln Lys Glu Asp Asn Ser Thr Tyr Ile Met Arg Val Leu  
 100 105 110  
 Lys Lys Thr Gly Asn Glu Gln Glu Trp Lys Ile Lys Leu Gln Val Leu  
 115 120 125  
 Asp Pro Val Pro Lys Pro Val Ile Lys Ile Glu Lys Ile Glu Asp Met  
 130 135 140  
 Asp Asp Asn Cys Tyr Leu Lys Leu Ser Cys Val Ile Pro Gly Glu Ser  
 145 150 155 160  
 Val Asn Tyr Thr Trp Tyr Gly Asp Lys Arg Pro Phe Pro Lys Glu Leu  
 165 170 175  
 Gln Asn Ser Val Leu Glu Thr Thr Leu Met Pro His Asn Tyr Ser Arg  
 180 185 190  
 Cys Tyr Thr Cys Gln Val Ser Asn Ser Val Ser Ser Lys Asn Gly Thr  
 195 200 205  
 Val Cys Leu Ser Pro Pro Cys Thr Leu Ala Arg Ser Phe Gly Val Glu  
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 Trp Ile Ala Ser Trp Leu Val Val Thr Val Pro Thr Ile Leu Gly Leu  
 225 230 235 240  
 Leu Leu Thr

<210> 112  
 <211> 1040  
 <212> DNA  
 <213> Homo sapiens

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 tcatgggatt gtcctatgga gcaatgtaaa cgtaactcaa ccagtataata ttttaagatg 540  
 gaaaatgatc ttccacaaaa aatacagtgt actcttagca atccattatt taatacaaca 600  
 tcatcaatca ttttgacaac ctgtatccca agcagcggtc attcaagaca cagatatgca 660  
 cttataccca taccattagc agtaattaca acatgtattg tgctgtatat gaatgggtatt 720  
 ctgaaatgtg acagaaaacc agacagaacc aactccaatt gattggtaac agaagatgaa 780  
 gacaacagca taactaaatt attttaaaaa ctaaaaagcc atctgatttc tcatttgagt 840  
 attacaattt ttgaacaact gttggaaatg taacttgaag cagctgcttt aagaagaaat 900  
 acccactaac aaagaacaag cattagtttt ggctgtcatc aacttattat atgactaggt 960  
 gcttgctttt ttgttcagta aattgttttt actgatgatg tagatacttt tgtaaataaa 1020  
 tgtaaataatg tacacaagtg 1040

<210> 113  
 <211> 250  
 <212> PRT  
 <213> Homo sapiens

<400> 113  
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 20 25 30  
 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn  
 35 40 45  
 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala

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	85	90
Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp		95
	100	105
Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr		110
	115	120
Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile		125
	130	135
Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp		140
145 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys		155
	160	165
Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro		170
	175	180
Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser		185
	190	195
Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala		200
	205	210
Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys		215
225 Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn		220
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<212> DNA  
<213> Homo sapiens

<400> 114

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<213> Homo sapiens

<400> 115

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35 40 45	

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                                   85                                  90  
 Leu Gly Leu Leu Leu Ser Cys Leu Met Leu Gly Val Ala Val Ile Cys  
                                   100                                  105                                  110  
 Leu Gly Val Arg Tyr Leu Gln Val Ser Gln Gln Phe Gln Glu Gly Thr  
                                   115                                  120                                  125  
 Arg Ile Trp Glu Ala Thr Asn Ser Ser Leu Gln Gln Gln Leu Arg Glu  
                                   130                                  135                                  140  
 Lys Ile Ser Gln Leu Gly Gln Lys Glu Val Glu Gln Glu Ser Gln Lys  
                                   145                                  150                                  155  
 Glu Leu Ile Ser Ser Gln Asp Thr Leu Gln Glu Lys Gln Arg Thr His  
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 Lys Asp Thr Glu Gln Gln Leu Gln Ala Cys Gln Ala Glu Arg Ala Lys  
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 Thr Lys Glu Asn Leu Lys Thr Glu Glu Arg Arg Arg Asp Leu Asp  
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 Cys Phe Tyr Ile Ser His Thr Leu Arg Ser Leu Glu Glu Ser Gln Lys  
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                                   305                                  310                                  315                                  320  
 Asp Lys Ile Lys Lys Tyr Tyr Gln Lys Trp Lys Arg Thr Phe Ser Glu  
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<210> 117  
 <211> 195  
 <212> PRT  
 <213> Mus musculus

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35 40 45  
Gln Arg Leu Leu Glu His Pro Glu Pro His Thr Ala Glu Leu Gln Leu  
50 55 60  
Asn Leu Thr Val Pro Arg Lys Asp Pro Thr Leu Arg Trp Gly Ala Gly  
65 70 75 80  
Pro Ala Leu Gly Arg Ser Phe Thr His Gly Pro Glu Leu Glu Gly  
85 90 95  
His Leu Arg Ile His Gln Asp Gly Leu Tyr Arg Leu His Ile Gln Val  
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Thr Leu Ala Asn Cys Ser Ser Pro Gly Ser Thr Leu Gln His Arg Ala  
115 120 125  
Thr Leu Ala Val Gly Ile Cys Ser Pro Ala Ala His Gly Ile Ser Leu  
130 135 140  
Leu Arg Gly Arg Phe Gly Gln Asp Cys Thr Val Ala Leu Gln Arg Leu  
145 150 155 160  
Thr Tyr Leu Val His Gly Asp Val Leu Cys Thr Asn Leu Thr Leu Pro  
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<210> 118  
<211> 909  
<212> DNA  
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<210> 119  
<211> 302  
<212> PRT  
<213> Homo sapiens

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Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn  
35 40 45  
Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr  
50 55 60  
Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr  
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<400> 121
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<211> 261  
<212> PRT  
<213> Homo sapiens

<400> 123  
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Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg  
35 40 45  
Arg Leu Asp Lys Ile Glu Asp Gln Arg Asn Leu His Glu Asp Phe Val  
50 55 60  
Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser  
65 70 75 80  
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Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu  
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Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly  
130 135 140  
Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln  
145 150 155 160  
Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr  
165 170 175  
Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser  
180 185 190  
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195 200 205  
Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His  
210 215 220  
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn  
225 230 235 240  
Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe  
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Gly Leu Leu Lys Leu  
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<210> 124  
<211> 1879  
<212> DNA  
<213> Homo sapiens

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<210> 125  
<211> 400  
<212> PRT  
<213> Homo sapiens

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35      40      45
Ile Thr Ser Asp Pro Lys Ala Asp Ser Thr Gly Asp Gln Thr Ser Ala
50      55      60
Leu Pro Pro Ser Thr Ser Ile Asn Glu Gly Ser Pro Leu Trp Thr Ser
65      70      75      80
Ile Gly Ala Ser Thr Gly Ser Pro Leu Pro Glu Pro Thr Thr Tyr Gln
85      90      95
Glu Val Ser Ile Lys Met Ser Ser Val Pro Gln Glu Thr Pro His Ala
100     105     110
Thr Ser His Pro Ala Val Pro Ile Thr Ala Asn Ser Leu Gly Ser His
115     120     125
Thr Val Thr Gly Gly Thr Ile Thr Thr Asn Ser Pro Glu Thr Ser Ser
130     135     140
Arg Thr Ser Gly Ala Pro Val Thr Thr Ala Ala Ser Ser Leu Glu Thr
145     150     155     160
Ser Arg Gly Thr Ser Gly Pro Pro Leu Thr Met Ala Thr Val Ser Leu
165     170     175
Glu Thr Ser Lys Gly Thr Ser Gly Pro Pro Val Thr Met Ala Thr Asp
180     185     190
Ser Leu Glu Thr Ser Thr Gly Thr Thr Gly Pro Pro Val Thr Met Thr
195     200     205
Thr Gly Ser Leu Glu Pro Ser Ser Gly Ala Ser Gly Pro Gln Val Ser
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Ser Val Lys Leu Ser Thr Met Met Ser Pro Thr Thr Ser Thr Asn Ala
225     230     235     240
Ser Thr Val Pro Phe Arg Asn Pro Asp Glu Asn Ser Arg Gly Met Leu
245     250     255
Pro Val Ala Val Leu Val Ala Leu Leu Ala Val Ile Val Leu Val Ala
260     265     270
Leu Leu Leu Leu Trp Arg Arg Arg Gln Lys Arg Arg Thr Gly Ala Leu
275     280     285
Val Leu Ser Arg Gly Gly Lys Arg Asn Gly Val Val Asp Ala Trp Ala
290     295     300
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Asp Ala Pro Ala Pro Asp Glu Pro Glu Gly Gly Asp Gly Ala Ala Pro  
385 390 395 400

<210> 126  
<211> 3567  
<212> DNA  
<213> Homo sapiens

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<212> PRT  
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Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu  
50 55 60  
Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ser  
65 70 75 80  
Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu  
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Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr  
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Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp  
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130 135 140  
Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala  
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Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Val Pro Pro  
165 170 175  
Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro  
180 185 190  
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195 200 205  
Arg Gly Pro Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser  
210 215 220  
Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp  
225 230 235 240  
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Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu  
260 265 270  
Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly  
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Gly Trp Lys Val Ser Ala Val Thr Leu Ala Tyr Leu Ile Phe Cys Leu  
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 355 360 365  
 Ala Gly Leu Gly Gly Thr Ala Pro Ser Tyr Gly Asn Pro Ser Ser Asp  
 370 375 380  
 Val Gln Ala Asp Gly Ala Leu Gly Ser Arg Ser Pro Pro Gly Val Gly  
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 Pro Glu Glu Glu Glu Gly Glu Gly Tyr Glu Glu Pro Asp Ser Glu Glu  
 405 410 415  
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 420 425 430  
 Ser Gln Asp Gly Ser Gly Tyr Glu Asn Pro Glu Asp Glu Pro Leu Gly  
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 450 455 460  
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 465 470 475 480  
 Pro His Gly Ser Ala Trp Asp Pro Ser Arg Glu Ala Thr Ser Leu Gly  
 485 490 495  
 Ser Gln Ser Tyr Glu Asp Met Arg Gly Ile Leu Tyr Ala Ala Pro Gln  
 500 505 510  
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 <212> DNA  
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Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile  
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305
Glu Glu Val Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val
325
Gln Ile Leu His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu
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Cys Met Ser Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His
355
Asn Gly Lys Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro
370
Lys Ile Leu Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn
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Ile Leu Gly Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln
405
Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile
420
Arg Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn
435
Pro Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu
450
Pro Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr
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Thr Ile Ala Cys Ala Arg Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro
485
Val Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys
500
Ile Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln
515
Cys Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu
530
Lys Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser
545
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Ile Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala
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Gly Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val
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Ser His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro His His
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Ser Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala
645
Tyr Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu
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Ser Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val
675
Ala Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys
690
Gly Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly
705
Leu Gln Glu Asn Ser Gly Gln Ser Phe Val Arg Asn Lys Lys
725
Val Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr
740
Asn Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro
755
Glu Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln
770
Arg Pro Pro Arg Thr Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His
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Lys Arg Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu
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 835 840 845

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 <212> DNA  
 <213> Homo sapiens

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 ccagggctgc agcaagcact caacggaatg gccctcctcg gagacacagc catgcatgtg 180  
 ccggcgggct ccgtggccag ccacctgggg accacgagcc gcagctatatt ctatttgacc 240  
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 cagaggacgg actccattcc caactcacct gacaacgtcc ccctcaaagg aggaaattgc 360  
 tcagaagacc tcttatgtat cctgaaaaga gctccattca agaagtcag ggccctacctc 420  
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 ggagtcagat atcaggatgg gaatctgggt atccaattcc ctggtttgta cttcatcatt 540  
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 aatgtgttgt ccatcttctt atacagtaat tcagactgaa cagtttctct tggccttcag 840  
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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg  
 50 55 60  
 Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly  
 65 70 75 80  
 Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys  
 85 90 95  
 Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys  
 100 105 110  
 Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp  
 115 120 125  
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Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln		
	180	185
Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val		
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Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val		
	210	215
Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp		
225	230	

<210> 136  
<211> 1125  
<212> DNA  
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<400> 136

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<210> 137  
<211> 281  
<212> PRT  
<213> Homo sapiens

<400> 137

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35 40 45	
Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser	
50 55 60	
Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu	
65 70 75 80	
Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu	
85 90 95	
Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg	
100 105 110	
Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln	
115 120 125	
Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp	
130 135 140	
Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp	
145 150 155 160	
Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg	
165 170 175	

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210 215 220  
Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn  
225 230 235 240  
Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu  
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<211> 2220  
<212> DNA  
<213> Homo sapiens

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<212> PRT  
<213> Homo sapiens

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50 55 60  
Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu  
65 70 75 80  
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85 90 95  
Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile  
100 105 110  
Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu  
115 120 125  
Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro  
130 135 140  
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145 150 155 160  
Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys  
165 170 175  
Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val  
180 185 190  
Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro  
195 200 205  
Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Tyr Ile Ser Pro Lys  
210 215 220  
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225 230 235 240  
Ser Val Thr Met Thr Cys Ser Ser Glu Gly Leu Pro Ala Pro Glu Ile  
245 250 255  
Phe Trp Ser Lys Lys Leu Asp Asn Gly Asn Leu Gln His Leu Ser Gly  
260 265 270  
Asn Ala Thr Leu Thr Leu Ile Ala Met Arg Met Glu Asp Ser Gly Ile  
275 280 285  
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290 295 300  
Glu Leu Ile Val Gln Glu Lys Pro Phe Thr Val Glu Ile Ser Pro Gly  
305 310 315 320  
Pro Arg Ile Ala Ala Gln Ile Gly Asp Ser Val Met Leu Thr Cys Ser  
325 330 335  
Val Met Gly Cys Glu Ser Pro Ser Phe Ser Trp Arg Thr Gln Ile Asp  
340 345 350  
Ser Pro Leu Ser Gly Lys Val Arg Ser Glu Gly Thr Asn Ser Thr Leu  
355 360 365  
Thr Leu Ser Pro Val Ser Phe Glu Asn Glu His Ser Tyr Leu Cys Thr  
370 375 380  
Val Thr Cys Gly His Lys Lys Leu Glu Lys Gly Ile Gln Val Glu Leu  
385 390 395 400  
Tyr Ser Phe Pro Arg Asp Pro Glu Ile Glu Met Ser Gly Gly Leu Val  
405 410 415  
Asn Gly Ser Ser Val Thr Val Ser Cys Lys Val Pro Ser Val Tyr Pro  
420 425 430  
Leu Asp Arg Leu Glu Ile Glu Leu Leu Lys Gly Glu Thr Ile Leu Glu  
435 440 445  
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450 455 460  
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465 470 475 480  
Leu Val Cys Gln Ala Lys Leu His Ile Asp Asp Met Glu Phe Glu Pro  
485 490 495  
Lys Gln Arg Gln Ser Thr Gln Thr Leu Tyr Val Asn Val Ala Pro Arg  
500 505 510  
Asp Thr Thr Val Leu Val Ser Pro Ser Ser Ile Leu Glu Gly Ser  
515 520 525  
Ser Val Asn Met Thr Cys Leu Ser Gln Gly Phe Pro Ala Pro Lys Ile  
530 535 540  
Leu Trp Ser Arg Gln Leu Pro Asn Gly Glu Leu Gln Pro Leu Ser Glu  
545 550 555 560  
Asn Ala Thr Leu Thr Leu Ile Ser Thr Lys Met Glu Asp Ser Gly Val

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 Cys Gly Asn Val Pro Glu Thr Trp Ile Ile Leu Lys Lys Lys Ala Glu  
 Thr Gly Asp Thr Val Leu Lys Ser Ile Asp Gly Ala Tyr Thr Ile Arg  
 Lys Ala Gln Leu Lys Asp Ala Gly Val Tyr Glu Cys Glu Ser Lys Asn  
 Lys Val Gly Ser Gln Leu Arg Ser Leu Thr Leu Asp Val Gln Gly Arg  
 Glu Asn Asn Lys Asp Tyr Phe Ser Pro Glu Leu Leu Val Leu Tyr Phe  
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<210> 140  
 <211> 2986  
 <212> DNA  
 <213> Homo sapiens

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 <212> PRT  
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 Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu Val Thr Cys  
 35 40 45  
 Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu Thr Pro Leu  
 50 55 60  
 Pro Lys Lys Glu Leu Leu Pro Gly Asn Asn Arg Lys Val Tyr Glu  
 65 70 75 80  
 Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr Ser Asn Cys  
 85 90 95  
 Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val Tyr Trp Thr  
 100 105 110  
 Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly  
 115 120 125  
 Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala Pro Arg Ala  
 130 135 140  
 Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu  
 145 150 155 160  
 Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val Leu Val Arg  
 165 170 175  
 Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu  
 180 185 190  
 Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln  
 195 200 205  
 Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu Val Ser Pro  
 210 215 220  
 Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp  
 225 230 235 240  
 Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp  
 245 250 255  
 Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala  
 260 265 270  
 Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu  
 275 280 285  
 Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr  
 290 295 300  
 Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu Thr Lys Pro  
 305 310 315 320  
 Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro  
 325 330 335  
 Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro  
 340 345 350  
 Arg Ala Gln Leu Leu Lys Ala Thr Pro Glu Asp Asn Gly Arg Ser  
 355 360 365  
 Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys  
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 420 425 430  
 Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val Thr Val Thr  
 435 440 445  
 Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser Thr Gln Gly  
 450 455 460  
 Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro Arg Tyr Glu  
 465 470 475 480  
 Ile Val Ile Ile Thr Val Val Ala Ala Val Ile Met Gly Thr Ala  
 485 490 495  
 Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr  
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 <212> DNA  
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 35 40 45  
 Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu  
 50 55 60  
 Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala  
 65 70 75 80  
 Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr  
 85 90 95  
 Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr  
 100 105 110  
 Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr  
 115 120 125  
 Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val  
 130 135 140  
 Phe Tyr Leu Thr Leu Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln  
 145 150 155 160  
 Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu  
 165 170 175  
 Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys  
 180 185 190  
 Thr Glu Thr Val  
 195